

SEQ 102543

Access DB#

SEARCH REQUEST FORM

TEXT 102949

Scientific and Technical Information Center

CRFE

Requester's Full Name: BAD-THUY NGUYEN Examiner #: 73403 Date: 8/27/03
 Art Unit: 1041 Phone Number 308-4243 Serial Number: 09/830,876
 Mail Box and Bldg/Room Location: TEOS Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): JOHN H. SKERRITT

Earliest Priority Filing Date: 11/11/1998

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

please search antibody that bind to SEQ ID 1-3
 of alpha-amylase

Inventor

AA
 1-15
 2-10
 3-10

thank you

66
 61
 02

STAFF USE ONLY

| | | |
|--|--------------------------|-----------------------------------|
| Searcher: <u>Hanly</u> | Type of Search | Vendors and cost where applicable |
| Searcher Phone #: _____ | NA Sequence (#) _____ | STN <u>P238</u> |
| Searcher Location: _____ | AA Sequence (#) <u>3</u> | Dialog _____ |
| Date Searcher Picked Up: _____ | Structure (#) _____ | Questel/Orbit _____ |
| Date Completed: <u>9/3</u> | Bibliographic _____ | Dr.Link _____ |
| Searcher Prep & Review Time: <u>SEQ:8 STN:25</u> | Litigation _____ | Lexis/Nexis _____ |
| Clerical Prep Time: _____ | Fulltext _____ | Sequence Systems <u>02</u> |
| Online Time: <u>Seq 8 STN 17</u> | Patent Family _____ | WWW/Internet _____ |
| | Other <u>11</u> | Other (specify) _____ |

PTO-1590 (8-01)

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



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(FILE 'HOME' ENTERED AT 11:12:37 ON 03 SEP 2003)

FILE 'CAPLUS' ENTERED AT 11:12:46 ON 03 SEP 2003

L1 207 S SKERRITT J?/AU
 L2 69 S L1 AND (CEREAL OR GRAIN)
 L3 17614 S ALPHA-AMYLASE OR .ALPHA.AMYLASE OR .ALPHA. AMYLASE
 L4 3 S L2 AND L3 *related to instant application*
 L5 53 S L2 AND ANTIBOD? *includes L4 cites*
 SELECT RN L4 1-3

FILE 'REGISTRY' ENTERED AT 11:17:41 ON 03 SEP 2003

L6 6 S E1-6 *6 cpds from L4 cites*

FILE 'CAPLUS' ENTERED AT 11:18:52 ON 03 SEP 2003

FILE 'REGISTRY' ENTERED AT 11:19:24 ON 03 SEP 2003

L7 4 S L6 NOT CL/ELS *getting rid of calc salts*

FILE 'CAPLUS' ENTERED AT 11:19:53 ON 03 SEP 2003

L8 3 S L7 AND L4 *3 cites w/ 4 cpds displayed*
 L9 51 S L5 NOT L4 *51 cites*

FILE 'REGISTRY' ENTERED AT 11:21:39 ON 03 SEP 2003

L10 1 S IDALVSIRTRGQIHS/SQSP *← Seq ID 1*
 L11 35 S CRDDRPYADG/SQSP *← Seq ID 2*
 L12 7 S VNWNKVGGG/SQSP *← Seq ID 3*
searched as exact & embedded sequences

FILE 'CAPLUS' ENTERED AT 11:24:50 ON 03 SEP 2003

L13 1 S L10
 L14 5 S L11
 L15 3 S L12
 L16 1 S L13-15 AND ANTIBOD? *1 cite mentions antibodies*

FILE 'USPATFULL' ENTERED AT 11:25:44 ON 03 SEP 2003

L17 0 S L10
 L18 0 S L11
 L19 0 S L12

FILE 'CAPLUS' ENTERED AT 11:26:03 ON 03 SEP 2003

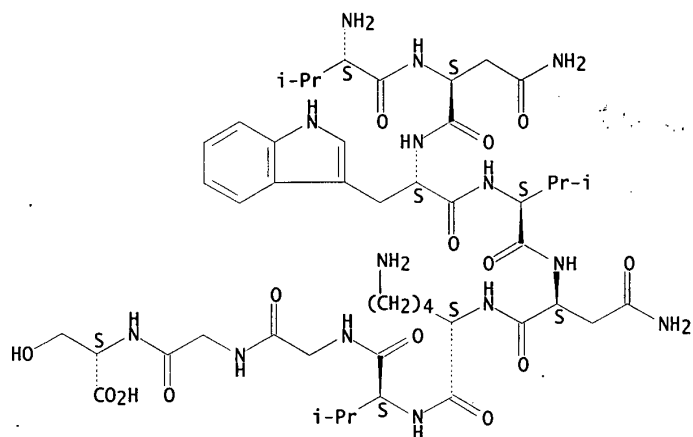
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=> d sqide 17

L7 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
 RN 268202-96-6 REGISTRY
 CN L-Serine, L-valyl-L-asparaginy1-L-tryptophyl-L-valyl-L-asparaginy1-L-lysyl-L-valylglycylglycyl- (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 10

SEQ 1 VNVVNVKVGGS
 MF C47 H74 N14 O14
 SR CA
 LC STN Files: CA, CAPLUS

Absolute stereochemistry.



1 REFERENCES IN FILE CA (1937 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d sqide 17 2

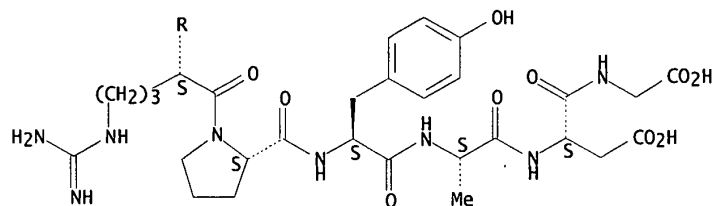
L7 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
 RN 268202-95-5 REGISTRY
 CN Glycine, L-cysteinyl-L-arginyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE; STEREOSEARCH
 SQL 10

SEQ 1 CRDDRPYADG
 MF C46 H70 N16 O18 S
 SR CA
 LC STN Files: CA, CAPLUS

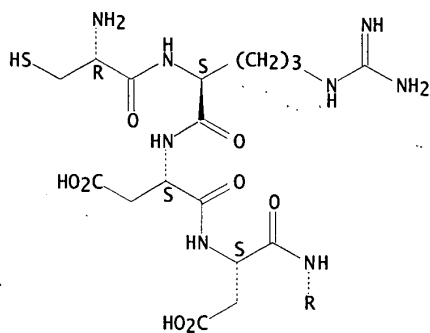
Absolute stereochemistry.

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PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

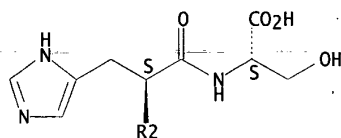
=> d sqide 17 3

L7 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 268202-94-4 REGISTRY
CN L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-
L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutaminy-L-isoleucyl-
L-histidyl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 15

SEQ 1 IDALVSIRTR GQIHS
MF C71 H124 N24 O22
SR CA
LC STN Files: CA, CAPLUS

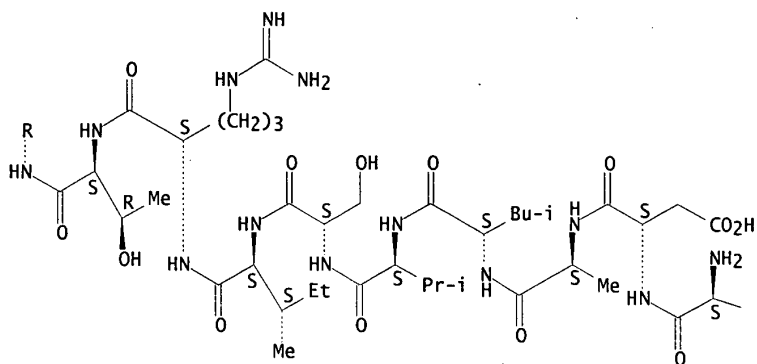
Absolute stereochemistry.

PAGE 1-A



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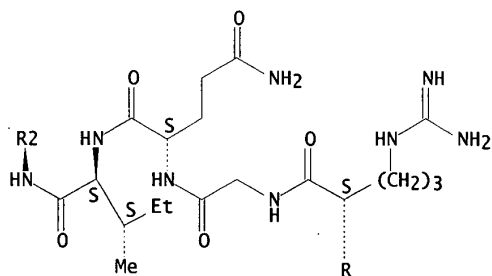
PAGE 2-A



PAGE 2-B



PAGE 3-A



1 REFERENCES IN FILE CA (1937 TO DATE)
1 REFERENCES IN FILE CAPLUS (1937 TO DATE)

=> d 17 4

L7 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9000-90-2 REGISTRY
CN Amylase, .alpha.- (9CI) (CA INDEX NAME)

Searched by Susan Hanley 305-4053

Page 3

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OTHER NAMES:

CN .alpha.-Amylase
 CN 1,4-.alpha.-D-Glucan glucanohydrolase
 CN 1,4-.alpha.-D-Glucanase
 CN 1,4-.alpha.-Glucanase
 CN Amano AD 1
 CN Amylase AD
 CN Amylase THC 250
 CN Amylogal CS
 CN Amylolisin 5
 CN Amylopsin
 CN Amylosubtilin
 CN Aquazym 120L
 CN Aquazyme 240
 CN Bactosol TK
 CN Ban
 CN Ban (enzyme)
 CN BAN 120L
 CN BAN 240
 CN Ban 480L
 CN Beisol T 2090
 CN Biobake 40000
 CN Bioferm
 CN Bioferm P
 CN Bioprep TBS
 CN Biotex GT
 CN Biozyme A
 CN Biozyme F
 CN Brewers Amylique TS
 CN Buclamase
 CN Canalpha 1000P
 CN Canalpha 600L
 CN Canalpha 60P
 CN Clarase
 CN Denazyme SA 7
 CN Desize 160
 CN E.C. 3.2.1.1
 CN Ekikakoso 6T
 CN EMCEmaltex 1000
 CN Endoamylase
 CN FD Super
 CN Fortizyme
 CN Fungamyl
 CN Fungamyl 2500BG
 CN Fungamyl 300L
 CN Fungamyl 800L
 CN G 995
 CN G-zyme G 995
 CN G6-Amylase
 CN Gamalpha HT 120L
 CN Gemsize 4A

ADDITIONAL NAMES NOT AVAILABLE IN THIS FORMAT - Use FCN, FIDE, or ALL for
 DISPLAY

AR 9000-85-5, 152923-47-2, 152923-48-3, 152923-49-4
 DR 9001-95-0, 9036-05-9, 9077-78-5, 135319-50-5, 106009-10-3, 70356-39-7,
 144133-13-1

MF Unspecified

CI COM, MAN

LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,
 CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM,
 CSNB, DDFU, DIOGENES, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, MRCK*,
 MSDS-OHS, NAPRALERT, NIOSHTIC, PHARMASEARCH, PIRA, PROMT, RTECS*,
 TOXCENTER, USAN, USPAT2, USPATFULL

(*File contains numerically searchable property data)

Other Sources: DSL**, EINECS**, TSCA**

(**Enter CHEMLIST File for up-to-date regulatory information)

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NGUYEN 09/830,876

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

13729 REFERENCES IN FILE CA (1937 TO DATE)

207 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

13740 REFERENCES IN FILE CAPLUS (1937 TO DATE)

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=> d ibib abs hitrn 18 1-3

L8 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:53744 CAPLUS

DOCUMENT NUMBER: 137:120380

TITLE: Albumin polymorphism and mapping of a dimeric .
alpha.-amylase inhibitor in wheatAUTHOR(S): Singh, J.; Appels, R.; Sharp, P. J.; Skerritt, J.
H.CORPORATE SOURCE: Cooperative Research Centre for Quality Wheat Products
and Processes, North Ryde, NSW 2113, AustraliaSOURCE: Australian Journal of Agricultural Research (2001),
52(11&12), 1173-1179

CODEN: AJAE9; ISSN: 0004-9409

PUBLISHER: CSIRO Publishing

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Any new protein or DNA marker is potentially useful to add detail to already constructed genetic chromosome maps and may be valuable in breeding programs wherever polymorphism exists. Non-gluten proteins represent 15-20% of total wheat grain proteins. Isoelec. focusing of wheat (*Triticum aestivum* L. em Thell.) proteins on ultrathin gels showed high resolu. and was found to be a useful tool in the differentiation of wheat varieties. Seventeen hexaploid wheat varieties were screened to investigate polymorphism of albumin proteins using isoelec. focusing. Polymorphism was obsd. for albumin polypeptides of pI 5.20, 5.85, 6.25, and 7.1, and 8.0. The polymorphic protein of pI 7.1 was mapped by analyzing doubled haploid populations from the intervarietal crosses, Cranbrook Halberd and Synthetic Opata 85. This protein locus was designated as Iha-B1.2, and is located on the short arm of chromosome 3B.

IT 9000-90-2, .alpha.-Amylase

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(inhibitor WDA1-3; albumin polymorphisms and mapping of dimeric
.alpha.-amylase inhibitor WDA1-3 in wheat using
isoelec. focusing)

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:335649 CAPLUS

DOCUMENT NUMBER: 132:333681

TITLE: Detection of preharvest sprouting in cereal
grains by immunoassay of .alpha.-
amylase

INVENTOR(S): Skerritt, John Howard

PATENT ASSIGNEE(S): Quality Wheat CRC Limited, Australia

SOURCE: PCT Int. Appl., 51 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|------------|
| WO 2000028319 | A1 | 20000518 | WO 1999-AU995 | 19991111 |
| W: AU, CA, JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| CA 2345403 | AA | 20000518 | CA 1999-2345403 | 19991111 |
| EP 1137935 | A1 | 20011004 | EP 1999-957719 | 19991111 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI | | | | |
| JP 2002529735 | T2 | 20020910 | JP 2000-581446 | 19991111 |
| AU 757926 | B2 | 20030313 | AU 2000-15341 | 19991111 |
| PRIORITY APPLN. INFO.: | | | AU 1998-7058 | A 19981111 |

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WO 1999-AU995 W 19991111

AB A two-site immunoassay for the qual. or quant. detection of .alpha.-amylase in a test sample comprises: (i) exposing the test sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .alpha.-amylase under conditions permitting binding; (ii) subsequently exposing bound .alpha.-amylase to a second ("detection") antibody or antibody fragment which specifically or preferentially binds to a second epitope on the .alpha.-amylase that is distinct from the first epitope, under conditions permitting binding of the second antibody or its fragment to the bound .alpha.-amylase; and (iii) detecting any binding of the second antibody or its fragment to the bound .alpha.-amylase, wherein either of the first or second epitopes is an epitope comprising one or more of the amino acid sequences: IDRLVSIRTRGQIHS, CRDDRYPYADG, or VNVVNKVGGS and variants thereof showing .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay is useful for detecting weather damage (i.e., preharvest sprouting) in cereal grain. Thus, a rapid tube sandwich ELISA detected .alpha.-amylase in preharvest-sprouted wheat exts. at .apprx.4 ng/mL.

IT 9000-90-2, .alpha.-Amylase 268202-94-4
268202-95-5 268202-96-6

RL: ANT (Analyte); ANST (Analytical study)
(detection of preharvest sprouting in cereal grains
by immunoassay of .alpha.-amylase)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
RECORD; ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:636830 CAPLUS

DOCUMENT NUMBER: 131:335982

TITLE: Development of a field enzyme-linked immunosorbent
assay (ELISA) for detection of .alpha.-
amylase in preharvest-sprouted wheat

AUTHOR(S): Verity, J. Christiana K.; Hac, Luch; Skerritt,
John H.

CORPORATE SOURCE: Quality Wheat CRC Ltd. and CSIRO Plant Industry,
Canberra, ACT 2601, Australia

SOURCE: Cereal Chemistry (1999), 76(5), 673-681
CODEN: CECHAF; ISSN: 0009-0352

PUBLISHER: American Association of Cereal Chemists

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A sandwich ELISA was developed for detection of .alpha.-amylase in preharvest sprouted wheat and adapted to rapid field-use formats requiring 15-20 min to perform. Polyclonal and monoclonal antibodies were prepd. to detect a mixt. of high and low pI isoenzymes of .alpha.-amylase and high pI isoenzymes only. All antibodies detected .alpha.-amylase on immunoblots of either a crude wheat ext. or of purified enzyme, but only the polyclonal antibodies functioned in a sandwich ELISA. Depending on the antibody combination, the tube ELISA detected either the high and low pI isoenzymes of .alpha.-amylase or the high pI isoenzymes only with a detection limit of .apprx.0.5-1.0 ng/mL of amylase. Wheats with falling nos. (FN) of <350 s could be discriminated from sound wheats, with decreasing FN producing increasing assay color. Using 130 wheat grain samples, ELISA absorbances for detection of both high and low pI isoenzymes and of high pI isoenzymes only were highly pos. correlated with amylase enzyme activity and neg. correlated with FN. The correlations were similar for detection of both isoenzyme families and for detection of high pI isoenzymes only. Analyses of three sets of wheat samples from different environments demonstrated that the relationship between ELISA absorbance and FN had little dependence on wheat cultivar. The precision of sample anal. using the field ELISA was similar to the precision of FN test app.

IT 9000-90-2, .alpha.-Amylase

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NGUYEN 09/830,876

RL: ANT (Analyte); ANST (Analytical study)
(field ELISA for detection of α -amylase in
preharvest-sprouted wheat)

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L9 ANSWER 1 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2002:397370 CAPLUS
DOCUMENT NUMBER: 138:38254
TITLE: Simple ELISA Detection of a New Polymorphic Ha Locus Encoded Protein
AUTHOR(S): Partridge, M. A. K.; Appels, R.; Skerritt, J. H.
CORPORATE SOURCE: CSIRO Plant Industry and Quality Wheat CRC Ltd, Canberra, 2601, Australia
SOURCE: Journal of Cereal Science (2002), 35(2), 189-200
CODEN: JCSCDA; ISSN: 0733-5210
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A rapid two-site sandwich ELISA was developed for detection of a previously uncharacterized protein encoded at the Ha locus on chromosome 5DS of wheat (*Triticum aestivum*). The assay used the combined specificity of two antibodies to detect a protein that was sol. in aq. alc., salt solns. and water. It was expressed in the endosperm of all soft wheats and *Triticum tauschii* accessions tested. The ELISA was highly specific, with no signal obtained with varieties that did not express the protein. The presence of the 5DS-encoded protein correlated with a significant change in both water absorption and av. hardness and particle size indexes in a doubled haploid population derived from a cross between cvs. Cranbrook.times.Halberd. Only some hard varieties expressed this protein indicating that the protein is not predictive for hardness. However, it may be a new factor, or a marker for a new factor, affecting kernel texture. A polypeptide of Mr 66 000 was purified from an ext. of Halberd flour by immunoaffinity chromatog. Its N-terminal amino acid sequence identified it as an albumin with high homol. to both mammalian serum albumins and sucrose synthase from a range of cereals. The assay may be valuable in wheat breeding programs for assessing kernel texture where the parents are of different ELISA phenotype, or for varietal identification, as the expression of the polypeptide is variable in hard wheat varieties.

REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:76313 CAPLUS
DOCUMENT NUMBER: 134:251498
TITLE: A new candidate protein for high lysine content in wheat grain
AUTHOR(S): Singh, Jaswinder; Sharp, Peter J.; Skerritt, John H.
CORPORATE SOURCE: CSIRO Plant Industry and Quality Wheat CRC Ltd, Canberra, 2601, Australia
SOURCE: Journal of the Science of Food and Agriculture (2001), 81(2), 216-226
CODEN: JSFAAE; ISSN: 0022-5142
PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Translation elongation factor 1.alpha. (EF-1.alpha.) from cereal embryo was recently reported to be rich in lysine, and the possibility of using this protein as a marker for feed quality was explored in maize. In this study we used immunochem. methods to investigate the relationship between the content of EF-1.alpha. and other proteins from wheat germ and lysine content in both hexaploid (bread) wheats and diploid wheat progenitors to the wheat A-genome. The levels of grain lysine, as well as their variation between lines or cultivars, were greater for the diploid wheats. While there was a significant correlation between the levels of EF-1.alpha. and grain lysine content, the binding of antibodies to a protein of Mr 37000 showed a higher correlation. This protein was characterized by amino acid sequencing as fructose

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1,6-bisphosphate aldolase. The possibility of using fructose
1,6-bisphosphate aldolase as a marker for feed quality and development of
a simple ELISA for quantification of lysine in wheat is demonstrated.
REFERENCE COUNT: 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 2000:161331 CAPLUS
DOCUMENT NUMBER: 132:206946
TITLE: Discrimination of glutenin subunits of wheat
INVENTOR(S): Giersch, Thomas Mario; Skerritt, John Howard
; Hill, Amanda Susanne
PATENT ASSIGNEE(S): Quality Wheat Crc Limited, Australia
SOURCE: PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|------------|
| WO 2000012557 | A1 | 20000309 | WO 1999-AU690 | 19990827 |
| W: AU, CA, JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| AU 9956116 | A1 | 20000321 | AU 1999-56116 | 19990827 |
| PRIORITY APPLN. INFO.: | | | AU 1998-5548 | A 19980828 |
| | | | WO 1999-AU690 | W 19990827 |

AB **Antibodies** and immunoassays are disclosed for discriminating
different high mol. wt. glutenin subunits (HMW-GS) in wheat. The
antibodies and immunoassays allow for the identification of
preferred cultivars in plant breeding and for detn. of HMW-GS in wheat
grain sample such as meal, flour and wheat grain ext.
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:80631 CAPLUS
DOCUMENT NUMBER: 128:165067
TITLE: Identification and characterization of U.S. wheats
carrying null alleles at the wx loci
AUTHOR(S): Graybosch, R. A.; Peterson, C. J.; Hansen, L. E.;
Rahman, S.; Hill, A.; Skerritt, J. H.
CORPORATE SOURCE: USDA-ARS, University of Nebraska, Lincoln, NE, 68583,
USA
SOURCE: Cereal Chemistry (1998), 75(1), 162-165
CODEN: CECHAF; ISSN: 0009-0352
PUBLISHER: American Association of Cereal Chemists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Granule-bound starch synthase (GBSS) is the primary enzyme responsible for
the synthesis of amylose in amyloplasts of cereal endosperm
cells. Bread wheats, due to their hexaploid genetic system, carry three
genes (wx loci) encoding GBSS. Purifn. and sepn. of GBSS from more than
200 North American hexaploid wheats allowed the indentification of
genotypes that carry null alleles at either the wx-A1 and wx-B1 loci. In
addn., the cultivar Ike carried both wx-A1 and wx-B1 null alleles. No
wx-D1 nulls were detected. Null alleles were found in 10% of the hard
winter wheats tested, but in only 2% of the samples soft winter wheats.
Amylose contents of wheats carrying single null alleles at either the
wx-A1 or wx-B1 loci often were lower than those of wild type wheats, but
greater redn. in amylose content was obsd. in Ike. Monoclonal
antibodies were used to quantify water-extractable GBSS in both
wild-type and null genotypes. Gene dosage compensation was evident,
although GBSS content, as measured by ELISA, was significantly lower in
Ike than in all other wheats. The indentification of null alleles in

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adapted genotypes suggests the development of wheats with a wide range of amylose contents will be possible by simple genetic crossing and selection.

REFERENCE COUNT: 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:703350 CAPLUS

DOCUMENT NUMBER: 127:356397

TITLE: Measurement of beta-amylase in malting barley (*Hordeum vulgare* L.). I. Development of a quantitative ELISA for beta-amylase

AUTHOR(S): Evans, D. E.; MacLeod, L. C.; Eglinton, J. K.; Gibson, C. E.; Zhang, X.; Wallace, W.; Skerrett, J. H.; Lance, R. C. M.

CORPORATE SOURCE: Dep. Plant Sci., Univ. Adelaide, Glen Osmond, SA 5064, Australia

SOURCE: Journal of Cereal Science (1997), 26(2), 229-239

CODEN: JCSCDA; ISSN: 0733-5210

PUBLISHER: Academic

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A double antibody, sandwich ELISA (ELISA) was developed using polyclonal antibodies specific to beta-amylase to est. the amt. of 'free' (sol. in aq. saline soln.) or 'combined' (extd. with saline soln. including reducing agent) beta-amylase protein in barley grain and malt. This ELISA was used to quantify the amt. of beta-amylase in barley grain and malt from four varieties grown at nine sites in South Australia in 1993. The antibody used to develop the ELISA reacted differently with beta-amylase dependent on whether the source was barley grain or malt, and on the beta-amylase band pattern in isoelec. focussing (IEF) of the barley variety. On the basis of their IEF band patterns barley varieties were divided into two types, designated Bmy1-Sd1 and Bmy1-Sd2. Malting resulted in proteolytic cleavage of the beta-amylase peptide with a redn. in the apparent mol. wt. of up to Mr 4000 and the appearance of new malt beta-amylase IEF bands that were more basic. The new malt beta-amylase IEF band patterns still allowed the identification of the Bmy1-Sd1 and Bmy1-Sd2 IEF types despite the change in mol. wt. and pI. The data obtained using the beta-amylase ELISA were highly correlated with beta-amylase activity for both the free and combined fractions when the IEF band pattern and its source, barley grain or malt, were taken into account.

L9 ANSWER 6 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:324233 CAPLUS

DOCUMENT NUMBER: 125:8895

TITLE: Rapid testing for insecticide residues in stored products using immuno- and enzyme- assays

AUTHOR(S): Skerrett, J. H.; Hill, A. S.; Edward, S. L.; Beasley, H. L.; Lee, N.; McAdam, D. P.; Rigg, A. J.

CORPORATE SOURCE: Division Plant Industry, CSIRO, Canberra, 2601, Australia

SOURCE: Stored Product Protection, Proceedings of the International Working Conference on Stored-Product Protection, 6th, Canberra, Aust., Apr. 17-23, 1994 (1994), Volume 2, 843-847. Editor(s): Highley, Ed. CAB International: Wallingford, UK.

CODEN: 62WJAN

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Accurate knowledge of the presence and levels of protectant residues in stored products is important for several reasons: for adequate control of possible infestation, to ensure that levels do not exceed legal Maximum Residue Limits, and to police specifications in sale/export contracts. While residue levels can be accurately detd. by gas-chromatog., the large no. of samples and sampling times required for thorough monitoring led us

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to develop an alternative method, suitable for on-site testing. Specific antibodies have been employed for the major grain protectants used in Australia and overseas: organophosphates (fenitrothion, chlorpyrifos-Me, pirimiphos-methyl), cabaryl, methoprene and synthetic pyrethroids (bioresmethrin, permethrin, phenothrin). Tests for deltamethrin and some other pyrethroids are under development. In addn., other grain protectant compds. such as malathion, methacrifos, dichlorvos, bromophos and etrimfos can be detected using a novel cholinesterase inhibition test. The reagents needed to perform the tests have been packaged into compact test kits, some of which are now com. available. All the immunoassay tests are performed in the same manner: grain or other commodity is extd. by blending in methanol, drops of the ext. added to an antibody-coated microwell or tube followed by drops of an enzyme conjugate soln. After a few minutes, the microwell or tube is washed in water to remove unbound components, then a color developer added. Different levels of protectant in the sample produce graded differences in yellow color. The cholinesterase test is performed similarly. Tests have been tuned for detection in the 0.05/ 0.1-10 ppm residue range in the commodity. Kits designed for simultaneous testing of a large no. of samples under lab. conditions have also been developed and are suitable for anal. of malted, baked or noodle end-products as well as raw grain. Insecticidal protectants are also important in developing countries. In a new collaboration with Indian scientists, we are extending this work to some other plant-based commodities and organochlorines, fungicides and other organophosphates. Advantages of immunoassay kits here will be the low capital and per-test costs.

L9 ANSWER 7 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1996:172786 CAPLUS
DOCUMENT NUMBER: 124:255671
TITLE: Cereal seed storage proteins
AUTHOR(S): Skerriitt, John H.; Tatham, Arthur S.
CORPORATE SOURCE: Division Plant Industry, CSIRO, Canberra, Australia
SOURCE: Structure of Antigens (1996), Volume 3, 349-86.
Editor(s): Van Regenmortel, M. H. V. CRC: Boca Raton, Fla.
CODEN: 57YWAS
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review with approx. 225 refs. Topics discussed include prolamins, evolutionary relationships of prolamins, methods of anal. of prolamins as antigens, epitope mapping approaches, structure of gluten polymers, and structure in relation to celiac toxicity and allergenicity.

L9 ANSWER 8 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:929212 CAPLUS
DOCUMENT NUMBER: 124:4892
TITLE: The major proteins of wheat endosperm starch granules
AUTHOR(S): Rahman, Sadequr; Kosar-Hashemi, Behjat; Samuel, Michael S.; Hill, Amanda; Abbott, David C.; Skerriitt, John H.; Preiss, Jack; Appels, Rudi; Morell, Matthew K.
CORPORATE SOURCE: Cooperative Research Centre for Plant Science, Canberra, 0200, Australia
SOURCE: Australian Journal of Plant Physiology (1995), 22(5), 793-803
CODEN: AJPPCH; ISSN: 0310-7841
PUBLISHER: Commonwealth Scientific and Industrial Research Organization
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Wheat starch contains two classes of assocd. proteins: proteins which are embedded within the granule and loosely assocd. surface proteins. The characterization of the major proteins that are embedded in the granule are described. Gel electrophoresis on the basis of size resolved these proteins into five bands of mol. wts. 60, 75, 85, 100 and 105 kDa. These

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polypeptides were demonstrated to be within the granule by their resistance to proteinase K digestion when granules were ungelatinized. The N-terminal sequences of these polypeptides are reported. The most prominent polypeptide is the 60 kDa granule-bound starch synthase. The N-terminal sequence obtained from the 75 kDa polypeptide shows homol. to rice sol. starch synthase. The 85 kDa band was resolved into at least two types of polypeptides, one of which reacted with polyclonal antiserum to the maize branching enzyme IIB. The 100 and 105 kDa polypeptides were located only in the granule and are related, on the basis of N-terminal sequence similarity and cross-reactivity to monoclonal **antibodies**. SDS-PAGE and monoclonal antibody cross-reactivity expts. suggest that the 100 and 105 kDa polypeptides are absent from starch granules from all other species examd., including other **cereals**. Thus, all the major granule proteins are involved in starch biosynthesis.

L9 ANSWER 9 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:58091 CAPLUS

DOCUMENT NUMBER: 122:8232

TITLE: Applications and limitations of immunochemical analysis of biopolymer quality in **cereals**

AUTHOR(S): Skerrett, J. H.; Andrews, J. L.; Blundell, M.; Beasley, H. L.; Bekes, F.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, Canberra, 2601, Australia
SOURCE: Food and Agricultural Immunology (1994), 6(2), 173-84
CODEN: FAIMEZ; ISSN: 0954-0105

PUBLISHER: Carfax

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 37 refs. The mixing and baking properties of wheaten doughs are detd. largely by the content, compn. and interactions of the major groups of flour proteins, the disulfide-bonded glutenin subunits and monomeric gliadins. Prediction of dough and bread quality is currently based on medium-scale rheol. and baking tests, but the slow throughput of such tests limits their use both by millers and baking companies and in early-generation screening by plant breeders. Thus identification and quantification of sp. flour proteins by immunoassay has the potential advantages of speed, simplicity and applicability to small samples in breeding. Tech. problems can arise from the low solubilities of these proteins and their high degrees of sequence homol. (which often give rise to extensive **antibody** cross-reaction). These problems can be minimized by modifications to methods and combining monoclonal **antibodies** with selected extn. conditions to enhance the functional specificity of the assay. Limitations also arise from attempting to predict the behavior of a complex system, in which mol. interactions and processing changes have been important, purely from flour polypeptide compn. The authors have used quant. immunoassays for sp. groups of glutenins and gliadins to predict aspects of dough strength and extensibility, while 'yes-no' direct enzyme-linked immunosorbent assays can be used to screen for products of particular wheat or translocated rye genes assocd. with sp. dough qualities. Monoclonal **antibodies** are also being employed to purify sp. flour proteins under non-denaturing conditions and in conjunction with novel very small scale dough testing equipment to directly assess functionality in doughs.

L9 ANSWER 10 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:34291 CAPLUS

DOCUMENT NUMBER: 122:104453

TITLE: Quality-related epitopes of high Mr subunits of wheat glutenin

AUTHOR(S): Andrews, J. L.; Skerrett, J. H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Cereal Science (1994), 19(3), 219-29
CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three hundred and eighty-four immobilized overlapping nonapeptides, corresponding to the full amino acid sequences of three high Mr subunits

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of glutenin from bread wheat (*Triticum aestivum*) grain, were used to det. the linear epitopes recognized by four monoclonal antibodies. These antibodies were selected on the basis of significant and pos. correlations between their binding to wheat flour exts. in a two-site (sandwich) enzyme immunoassay and rheol. measures of dough strength, an important aspect of bread wheat quality. The antibodies did not bind to a single, specific sequence but bound a series of related peptides in each high Mr glutenin subunit examd. The sequences recognized were not identical for the four antibodies, but in each case were in the central repeating domain of the high Mr glutenin subunits, and usually comprised regions that overlapped the degenerate repeat nonamer and hexamer sequences. High Mr glutenin subunits that have been assocd. with greater dough strength, such as the D-genome allelic products 1Dx5 and 1Dy10, displayed an increased no. of the epitope sequences. The location of the epitopes in sequences of overlapping .beta.-turns in the repetitive region supports the hypothesis that dough elasticity arises partly from .beta.-turn-forming secondary structure in the repeat regions of the Mr glutenin subunits. Addnl. .beta.-turns within high Mr subunits may extend their structure to allow increased interaction between the glutenin subunits and with the other proteins of the gluten complex, thus improving dough strength.

L9 ANSWER 11 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268438 CAPLUS
DOCUMENT NUMBER: 120:268438
TITLE: Improved immunoassay for chlorpyrifos-methyl (Reldan) in grain.
AUTHOR(S): Edward, Simone L.; Skerritt, John H.; Hill, Amanda S.; McAdam, David P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Food and Agricultural Immunology (1993), 5(3), 129-44
CODEN: FAIMEZ; ISSN: 0954-0105
DOCUMENT TYPE: Journal
LANGUAGE: English

AB An improved immunoassay for Reldan in grain was developed, based on an immobilized polyclonal antibody. This assay had greater sensitivity (limit of detection of 0.cntdot.02 ppm in grain, or 0.cntdot.05-0.cntdot.1 ppb in buffer), was less susceptible to interference from methanol (used to ext. the residue from grain) and had greater precision than the earlier monoclonal antibody assay (Skerritt, J.H., et al, 1992). The polyclonal antibody exhibited greater cross-reaction with chlorpyrifos-Et (not used as a grain protectant), but less with fenchlorphos and bromophos (used occasionally as grain protectants), and employed a more stable peroxidase conjugate than the monoclonal antibody assay. Good correlations were obtained between Reldan residue levels in wheat grain detd. by the improved immunoassay and by gas chromatog. The properties of the polyclonal antibody should also allow its use in a rapid field assay.

L9 ANSWER 12 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268419 CAPLUS
DOCUMENT NUMBER: 120:268419
TITLE: Rapid field tests for the organophosphorus pesticides, fenitrothion and pirimiphos-methyl--reliable estimates of residues in stored grain
AUTHOR(S): Beasley, H. L.; Skerritt, J. H.; Hill, A. S.; Desmarchelier, J. M.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Stored Products Research (1993), 29(4), 357-69
CODEN: JSTPAR; ISSN: 0022-474X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In order for grain handlers and traders to reliably est. residues of grain protectants in the field, antibody-based tests were developed for the organophosphorus pesticides,

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fenitrothion and pirimiphos-Me. To complement the rapid anal., rapid but efficient extn. techniques were developed. In these tests, a pesticide-contg. methanol ext. of the grain sample and an enzyme-labeled component are added dropwise to precoated tubes contg. buffer. After a brief incubation, the tubes are rinsed out in tap water and a substrate/chromogen for the enzyme is added. The color developed is stabilized by acidification and the test result read either by eye or in a portable field photometer. Significant levels of the particular pesticide result in a pale color compared to a dark green pesticide-free control. No calcs. were required to provide a quant. est. of residue as this could be read directly from a graph of color yield (absorbance) vs logarithm of pesticide concn., using std. solns. of pesticide. For fenitrothion, the test had a limit of detection of 4 ng/mL (0.1 ppm in grain) and gave quant. ests. in the range 0.5-15 ppm (in the grain), while the pirimiphos-Me test had a limit of detection of 1 ng/mL (0.03 ppm in grain) and gave quant. ests. over the range 0.1-15 ppm. Thus both tests can be used to segregate "pesticide-free" grain, with residues below 0.1 ppm. Data obtained using the field test correlated well with those obtained using lab. methods, including both gas-liq. chromatog. and immunoassay using microwell plates. The field immunoassay reagents were formatted into a small prototype test kit, and the components stabilized for field use.

L9 ANSWER 13 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:268414 CAPLUS

DOCUMENT NUMBER: 120:268414

TITLE: Analysis of the grain-protectant pesticides chlorpyrifos-methyl and methoprene with a 15-min immunoassay for field or elevator use

AUTHOR(S): Edward, Simone L.; Hill, Amanda S.; Ashworth, Paul; Matt, Jonathan; Skerrett, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, Australia

SOURCE: Cereal Chemistry (1993), 70(6), 748-52

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Antibody-based tests for field use have been developed to enable semiquant. anal. of two grain protectants, chlorpyrifos-Me and methoprene. In these tests, a pesticide-contg. methanol ext. of the pment.

L9 ANSWER 15 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1993:664564 CAPLUS

DOCUMENT NUMBER: 119:264564

TITLE: Quantitation of bioresmethrin, a synthetic pyrethroid grain protectant, by enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; McAdam, David P.; Edward, Simone L.; Skerrett, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, NSW 2113, UK

SOURCE: Journal of Agricultural and Food Chemistry (1993), 41(11), 2011-18

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An enzyme immunoassay was developed for the synthetic pyrethroid, bioresmethrin, by use of a novel approach for synthesis of the pyrethroid-protein hapten conjugate for antibody prepn. Bioresmethrin was hydrolyzed at the ester linkage, and following protection of the chrysanthemic acid group, the 2-methylprop-1-ene substituent was oxidatively cleaved. The newly formed and unprotected acid group was reesterified to the other bioresmethrin hydrolysis product [[2-(phenylmethyl)-4-furyl]-methanol], and following substitution of the protecting group, the hapten was coupled to either protein for antibody prodn. or peroxidase for use in the immunoassay. The most sensitive assay employed an antibody prepd. to a deriv. with a 4-carbon spacer arm between bioresmethrin and carrier protein, but used a bioresmethrin-enzyme reporter prepd. using a 4-

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(aminomethyl)cyclohexane-carboxylic acid spacer arm (limit of detection 2 ppb in buffer, 50 ppb in whole wheat or barley grain). Good correlations between HPLC and ELISA detns. of bioresmethrin in whole or ground barley grain were obtained. The sensitivity of the assay was slightly lower in ground grain or flour milling fractions due to interference from coextractives in methanol exts. Apart from resmethrin, of which bioresmethrin is the 1R,3R-trans-isomer, the assay did not detect a variety of other pyrethroids in com. use.

L9 ANSWER 16 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1993:537750 CAPLUS

DOCUMENT NUMBER: 119:137750

TITLE: A simple antibody-based test for dough strength. III. Further simplification and collaborative evaluation for wheat quality screening
AUTHOR(S): Andrews, John L.; Blundell, Malcolm J.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1993), 70(3), 241-6

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An antibody-based method for discrimination of wheat flours or whole meals on the basis of differences in dough strength (Skerritt 1991b), as measured by extensigraph max. resistance for example, was simplified for use in large-scale screening to predict dough quality. The major modification was the addn. of unlabeled antibody to the dild. grain ext. being analyzed, which simplified sample handling. It reduced the diln. of the grain exts. being tested and improved the differentiation between flours of different strengths. A method was also developed for simultaneous extn. and testing of sets of 96 unweighed whole meal samples. The method was tested in a collaboration trial in eight labs. (none with significant prior immunoassay experience) using two sep. analyses of a set of 16 flours, including three blind duplicates. Each lab. reported highly significant correlations between color developed in the assay and rheol. measurements of dough strength, such as farinograph development time and extensigraph max. resistance. Good ests. of within- and between-lab. precision were also obtained, indicating that the method was suitable for quality assessment in wheat breeding.

L9 ANSWER 17 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:488842 CAPLUS

DOCUMENT NUMBER: 117:88842

TITLE: Mono- and polyclonal antibodies to the organophosphate fenitrothion. 1. Approaches to hapten-protein conjugation

AUTHOR(S): McAdam, David P.; Hill, Amanda S.; Beasley, Helen L.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, Canberra, 2601, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(8), 1466-70

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three different chem. approaches were used to couple the organophosphorus pesticide fenitrothion to carrier proteins for prodn. of polyclonal and monoclonal antibodies. Hapten conjugates coupled through the pesticide phosphate group yielded the most-specific and highest affinity antibodies, although antibodies of moderate affinity were obtained by derivatization and coupling through the arom. nitro group following its redn. and amide formation with an adipic acid spacer arm. Assay formats using either immobilized antibody or immobilized hapten-protein conjugate could be used to det. free fenitrothion. The most sensitive assay could detect 1 ng of fenitrothion. It is recommended for the detection of residues of fenitrothion used for the protection of stored cereals.

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L9 ANSWER 18 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:488841 CAPLUS

DOCUMENT NUMBER: 117:88841

TITLE: Mono- and polyclonal antibodies to the organophosphate fenitrothion. 2. Antibody specificity and assay performance

AUTHOR(S): Hill, Amanda S.; Beasley, Helen L.; McAdam, David P.; Skerritt, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(8), 1471-4

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The performance and specificities of antibody-based assays for fenitrothion (I) were studied. I could be detected in grain in assays with either polyclonal or monoclonal antibodies using either immobilized antibody or immobilized hapten-protein conjugates. Most assay formats and antibodies distinguished I from structurally similar organophosphates, and variable extents of cross-reaction with metabolites were obsd. The concn. of I in wheat grain samples was measured in 3 assay formats with 2 antibodies, and in each case good correlations were obtained with the results obtained by gas-liq. chromatog. For routine use, a format detecting 3 ng and suitable for anal. over the range 100 ppb-20 ppm in grain was preferred.

L9 ANSWER 19 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:446860 CAPLUS

DOCUMENT NUMBER: 117:46860

TITLE: Enzyme-linked immunosorbent assay for quantitation of organophosphate pesticides: fenitrothion, chlorpyrifos-methyl, and pirimiphos-methyl in wheat grain and flour-milling fractions

AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; Beasley, Helen L.; Edward, Simone L.; McAdam, David P.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of AOAC International (1992), 75(3), 519-28

CODEN: JAINEE; ISSN: 1060-3271

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Simple, competitive enzyme-linked immunosorbent assays (ELISAs) were developed for the quantitation of each of 3 major organophosphate insecticides: fenitrothion (FN), chlorpyrifos-Me (CPM), and pirimiphos-Me (PIRM). The performance of these assays on wheat grain and (for FN and CPM) on milling fractions such as flour, wheat germ, and bran was assessed. Each assay was specific for the particular compd., i.e., no significant cross-reaction with the other 2 pesticides was obsd. Only limited reactions were noted with major metabolites or analogs of these pesticides. Assay limits of detection of 0.3 ng FN, 0.2 ng CPM, and 0.02 ng PIRM were recorded, corresponding to limits of detection in whole grain of 0.08 ppm FN, 0.2 ppm CPM, and 0.03 ppm PIRM. Each compd. in grain and milling fractions could be extd. quant. by shaking in MeOH. Multiresidue anal. of the 3 insecticides was performed by simultaneously adding the cereal ext. (dild. in phosphate buffer) to sep. duplicate microwells coated with antibodies to FN, CPM, and PIRM and adding appropriate pesticide-horseradish peroxidase conjugates. High correlations between gas chromatog. and the ELISA methods were obtained for insecticide levels in whole wheat and in milling fractions. The ELISA assays had precision similar to those of instrumental pesticide analyses.

L9 ANSWER 20 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:446838 CAPLUS

DOCUMENT NUMBER: 117:46838

TITLE: Analysis of the synthetic pyrethroids, permethrin and

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1(R)-phenothrin, in grain using a monoclonal antibody-based test
 AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; McAdam, David P.; Stanker, Larry H.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
 SOURCE: Journal of Agricultural and Food Chemistry (1992), 40(7), 1287-92
 CODEN: JAFCAU; ISSN: 0021-8561
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A monoclonal antibody generated to the synthetic pyrethroid-related hapten, (3-phenoxybenzyl)-2,2-dimethylcyclopropane-1,3-dicarboxylate-protein conjugate, was used to develop assays for detg. permethrin and 1(R)-phenothrin in wheat grain and flour milling fractions. The earlier 3-h assay was simplified by using 2 approaches. The antibody was directly conjugated to the enzyme horseradish peroxidase (HRP), which eliminated a sep. incubation and washing step from the assay. Also, an assay was developed with microwell-bound monoclonal antibody and a HRP-labeled 3-phenoxybenzoic acid deriv. These assay formats have advantages in increased sensitivity and, in the case of the latter assay, accuracy with grain and flour samples. The most sensitive assay format could detect 1.5 ng/mL permethrin; 50% inhibition of antibody binding occurred at 10 ng/mL. These values corresponded to 75 ppb and 500 ppb, resp., in the original wheat sample. MeOH was the most effective pyrethroid extractant. Use of a simple cleanup procedure for ground grain exts. improved ELISA accuracy but could be omitted for screening purposes.

L9 ANSWER 21 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1992:127228 CAPLUS
 DOCUMENT NUMBER: 116:127228
 TITLE: Cellular and humoral responses in celiac disease. 2. Protein extracts from different cereals
 AUTHOR(S): Skerritt, John H.; Devery, Jannine M.; Penttila, Imme A.; LaBrooy, Justin T.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
 SOURCE: Clinica Chimica Acta (1991), 204(1-3), 109-22
 CODEN: CCATAR; ISSN: 0009-8981
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB The humoral and cellular immune responses to grain protein exts. from celiac-toxic and non-toxic cereals were compared by use of a no. of ELISA and immunoblotting methods and the indirect leukocyte migration inhibition factor (LMIF) assay. Both adult and child celiacs had elevated levels of serum antibody to proteins from the celiac-toxic cereals, namely bread wheat, durum wheat, rye and barley and low levels of proteins from other cereals. Using protein-blotting techniques, antibody binding was greatest to gliadins/low-mol.-mass glutenin subunits and homologous prolamins from rye and barley, consistent with the ELISA findings. Competition ELISA and preabsorption tests indicated that antibody reaction to maize storage proteins did not simply result from cross-reaction of antigliadin antibodies. In LMIF assays, only the wheat exts. had activity in celiac patients. This is most likely partly due to loss of some T-cell epitopes from the extn. technique required for these proteins, as well as the relatively small effects seen for even very active fractions in the LMIF assay.

L9 ANSWER 22 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1992:55602 CAPLUS
 DOCUMENT NUMBER: 116:55602
 TITLE: Immunocytochemical localization of wheat storage proteins in endosperm cells 30 days after anthesis
 AUTHOR(S): Stenram, Unna; Heneen, Waheeb K.; Skerritt, John H.
 CORPORATE SOURCE: Dep. Crop Genet. Breed., Swed. Univ. Agric. Sci., Svaloev, S-268 00, Swed.

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SOURCE: Journal of Experimental Botany (1991), 42(244), 1347-55
 CODEN: JEBOA6; ISSN: 0022-0957
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB Antisera against seven different wheat (*Triticum aestivum*) storage protein subfractions were characterized using (1) ELISA with gliadins and low- and high-mol. wt. glutenin subunits and (2) electrophoresis (SDS-PAGE and acidic buffer PAGE) and immunoblotting. The specificities of these antisera (polyclonal antibodies) and 13 monoclonal antibodies covered various patterns of reactivity with alpha-, beta-, gamma- and omega-gliadins and low- and high-mol. wt. glutenins. The antisera and antibodies were applied to ultrathin sections of wheat endosperm tissue, from kernels fixed 30 days after anthesis, and were detected by secondary antibodies tagged with either 5 or 15 nm gold particles using transmission electron microscopy. Labeling was denser when the small gold particles were used but irresp. of gold particle size, labeling of polyclonal antisera predominated when the endosperm cells were subjected to both mono- and polyclonal antibodies. Each of the antisera and monoclonal antibodies that labeled the protein bodies, labeled them more or less uniformly. This indicates that only one kind of protein body, contg. all gliadin and glutenin subfractions, exists during this stage of grain development. Electron-dense globular inclusions found in many protein bodies were not labeled. Label was also found on protein-like material present in the lumen of the rough endoplasmic reticulum and on vesicles of the Golgi app. Thus, concn. of storage proteins takes place both at the site of synthesis, the lumen of the rough endoplasmic reticulum, and at the site of processing and transport, the vesicles of the Golgi app. Fusions between these proteinaceous materials give rise to larger protein bodies and ultimately to the protein matrix.

L9 ANSWER 23 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1991:605926 CAPLUS
 DOCUMENT NUMBER: 115:205926
 TITLE: Monoclonal and polyclonal antibodies and test method for determination of fenitrothion and closely related organophosphates
 INVENTOR(S): Skerritt, John Howard; Hill, Amanda Susanne; McAdam, David Peter
 PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, Australia
 SOURCE: PCT Int. Appl., 30 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---|------|----------|-----------------|------------|
| WO 9100294 | A1 | 19910110 | WO 1990-AU278 | 19900629 |
| W: AU, CA, GB, JP, US | | | | |
| RW: AT, BE, CH, DE, DK, ES, FR, GB, IT, LU, NL, SE | | | | |
| CA 2062820 | AA | 19901231 | CA 1990-2062820 | 19900629 |
| CA 2062820 | C | 20021112 | | |
| AU 9058550 | A1 | 19910117 | AU 1990-58550 | 19900629 |
| AU 633113 | B2 | 19930121 | | |
| ZA 9005132 | A | 19911030 | ZA 1990-5132 | 19900629 |
| EP 479834 | A1 | 19920415 | EP 1990-909585 | 19900629 |
| EP 479834 | B1 | 19991110 | | |
| R: AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, LU, NL, SE | | | | |
| JP 04503760 | T2 | 19920709 | JP 1990-509255 | 19900629 |
| JP 08008874 | B4 | 19960131 | | |
| AT 186553 | E | 19991115 | AT 1990-909585 | 19900629 |
| US 5541079 | A | 19960730 | US 1994-300931 | 19940906 |
| PRIORITY APPLN. INFO.: | | | AU 1989-5018 | A 19890630 |

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WO 1990-AU278 A 19900629
US 1991-784389 B1 19911230

OTHER SOURCE(S): MARPAT 115:205926

AB Monoclonal and polyclonal **antibodies** and fragments thereof are described which are capable of binding to specific members or groups of O,O-dialkyl-O-(X) phosphorothioate compds. [X = (substituted) arom. or (substituted) heterocyclic group]. Hybridoma cell lines, methods for making **antibodies** and immunogens, and assays and kits including the **antibodies** are also disclosed. Thus, fenitrothion was converted to the diazonium salt and then conjugated with ovalbumin for prodn. of **antibodies**. The **antibodies** were used in a competitive enzyme immunoassay for fenitrothion in wheat.

L9 ANSWER 24 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:603551 CAPLUS

DOCUMENT NUMBER: 115:203551

TITLE: Chromosomal control of wheat gliadin protein epitopes: analysis with specific monoclonal **antibodies**

AUTHOR(S): Skerrett, J. H.; Martinuzzi, O.; Metakovskii, E. V.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Theoretical and Applied Genetics (1991), 82(1), 44-53
CODEN: THAGA6; ISSN: 0040-5752

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The genetic relationships between small clusters of monomeric alc.-sol. wheat (*Triticum aestivum* L.) grain storage proteins (gliadins) were studied using a panel of monoclonal **antibodies** and immunoblotting, ELISA, and RIA methods. Use of Chinese Spring nullisomic-tetrasomic lines showed that several narrow-specificity **antibodies** bound specifically to gliadins encoded by genes located on a single chromosome. In at least one case, **antibodies** bound to genetic blocks of gliadins, indicating that these block members have structural homol. However, often not all gliadins of a block were recognized by an **antibody**. For broad-specificity **antibodies** and some narrow-specificity **antibodies** structural genes on several chromosomes were important. Studies with several primitive wheat species indicated that, while **antibodies** usually bound gliadins from the same genome in bread and primitive wheats, **antibodies** sometimes bound proteins of quite differing mobilities in the two wheat types. Use of **antibodies** to identify gliadin blocks is simpler than block anal. based on performing crosses, and should be of value in monitoring genotype/end-use quality relationships.

L9 ANSWER 25 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:581642 CAPLUS

DOCUMENT NUMBER: 115:181642

TITLE: Determination of the insect growth regulator methoprene in wheat grain and milling fractions using an enzyme immunoassay

AUTHOR(S): Hill, Amanda S.; Mei, Joanne V.; Yin, Chih Ming; Ferguson, Bruce S.; Skerrett, John H.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Agricultural and Food Chemistry (1991), 39(10), 1882-6

CODEN: JAFCAU; ISSN: 0021-8561

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The enzyme immunoassay of J. V. Mei, et al. (1990) was improved for the insect growth regulator methoprene, and the assay was used to det. methoprene in whole wheat grain and milling fractions, including flours, whole meal, bran, and wheat germ. Either MeOH or MeCN could be used to ext. methoprene from grain, flours, and bran; no cleanup of exts. was required. MeOH produced less matrix effects and could be tolerated at higher concns. in the assay. MeCN gave more reliable results in the extn. of methoprene from wheat germ. The improved assay had a sensitivity of 250 pg/mL, and 50% inhibition of **antibody** binding

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occurred at 3 ng/mL, corresponding to a max. sensitivity of 60 ppb and 50% inhibition of antibody binding at 0.75 ppm in the wheat sample when the routine assay method was used. The latter value is in keeping with residue levels typically found in methoprene-treated stored grain. Good correlations were found between methoprene detd. in wheat and grain fractions by the enzyme immunoassay and by conventional HPLC anal.

L9 ANSWER 26 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:557244 CAPLUS
DOCUMENT NUMBER: 115:157244
TITLE: Testing cereal products and samples by immunoassay. Test for organophosphate, carbamate, and pyrethroid grain protectants
AUTHOR(S): Skerritt, John H.; Robson, Lisa G.; McAdam, David P.; Hill, Amanda S.
CORPORATE SOURCE: Div. Plant Ind., Commonw. Sci. and Ind. Res. Organ., North Ryde, 2113, Australia
SOURCE: ACS Symposium Series (1990), 451(Immunoassays Trace Chem. Anal.), 124-38
CODEN: ACSMC8; ISSN: 0097-6156
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Organophosphates, synthetic pyrethroids and/or carbaryl are applied to stored grain and grain storage facilities to minimize insect infestation. Local industry deregulation coupled with increasingly stringent export residue tolerances and consumer demand for chem.-free foods have markedly increased demand for pesticide residue testing. Monoclonal and polyclonal antibodies have been prep'd. and test methods developed for fenitrothion, the major organophosphate pesticide used on grain. Some antibodies were specific for fenitrothion and sensitive to 0.1-0.5 ng; other antibodies bound to closely related organophosphates as well. A simple cholinesterase inhibition test for general screening for organophosphates and carbamates is being adapted for use in field situations or high-throughput labs. Antibodies to certain pyrethroids (phenothrin, permethrin) are being assessed for use in simple test kits.

L9 ANSWER 27 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:534290 CAPLUS
DOCUMENT NUMBER: 115:134290
TITLE: Determination of gluten in foods using a monoclonal antibody-based competition enzyme immunoassay
AUTHOR(S): Hill, Amanda S.; Skerritt, John H.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Food and Agricultural Immunology (1990), 2(1), 21-35
CODEN: FAIMEZ; ISSN: 0954-0105
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A sensitive competition enzyme-immunoassay for quantification of gluten in foods was developed, using horseradish peroxidase-labeled monoclonal antibodies. Selected antibodies specific for wheat .omega.-gliadin components were used, and these antibodies bound proteins from the related cereals, rye and barley, which are also toxic to individuals with gluten-intolerance (coeliac disease). Binding of these antibodies was not inhibited by heating of gluten during cooking or baking and the assay did not detect cereals not toxic in coeliac disease, such as maize or rice. Gluten could be quantified at higher levels in meat products or in cereal products such as flours or baked goods. Results were not affected by wheat variety. Quant. results could be obtained using simple extrn. techniques and solvents (40% or 70% ethanol). Detection of gluten was quant. in a wide range of foods, except for certain products contg. gluten proteins that had been subjected to severe heat, enzymic, or chem. treatment. In these products overestimates rather than underestimates were usually obtained.

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L9 ANSWER 28 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:469981 CAPLUS
DOCUMENT NUMBER: 115:69981
TITLE: Immunology invades chemistry: testing cereals
with antibodies
AUTHOR(S): Skerritt, John H.; Hill, Amanda S.; McAdam,
David P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Chemistry in Australia (1990), 57(9), 297-300
CODEN: CHAUDY; ISSN: 0312-8180
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 11 refs. of immunochem. assays used in cereal
prodn. and processing, including detection of toxic, illegal, or quality
component evaluating wheat gluten strength, dough extensibility,
grain hardness, flour protein content and lipid and starch compn.,
variety identification, detection of pesticide residues, detection and
detn. of gluten in foods, and detection of chill-proofing enzymes in beer.

L9 ANSWER 29 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:183936 CAPLUS
DOCUMENT NUMBER: 114:183936
TITLE: Enzyme immunoassay for determination of gluten in
foods: collaborative study
AUTHOR(S): Skerritt, John H.; Hill, Amanda S.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal - Association of Official Analytical Chemists
(1991), 74(2), 257-64
CODEN: JANCA2; ISSN: 0004-5756
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A collaborative study was performed in 15 labs. to validate a monoclonal
antibody-based enzyme immunoassay (EIA) for detn. of gluten in
foods. The study included 13 samples: corn starch, gluten-free baking
mixes, wheat flours, cookies, cooked meats, and a soup. Gluten was
present in these samples at either zero or 0.02 to 10% by wt., i.e., over
almost 3 orders of magnitude. The mean assay values for the foods varied
from 88 to 105% of the actual amts. The assay was quant. for
cereal products and the soup with repeatability (RSDr, relative
std. deviation) and reproducibility (RSDR) of 16-22% and 24-33%, resp.
The assay was semiquant. for the processed meat products (RSDr 14 and 26%
and RSDR 46 and 56%), probably because gluten was unevenly distributed in
the small (1 g) samples that were analyzed. The ELISA method produced no
false pos. results, and false negatives obtained with tannin-contg. foods
could be avoided by use of a modified sample extractant. None of the
collaborators reported problems in following the protocol. The method has
been adopted official first action by AOAC for detn. of wheat gluten in
foods.

L9 ANSWER 30 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:78626 CAPLUS
DOCUMENT NUMBER: 114:78626
TITLE: Immunological homologies between wheat gluten and
starch granule proteins
AUTHOR(S): Skerritt, J. H.; Frend, A. J.; Robson, L.
G.; Greenwell, P.
CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia
SOURCE: Journal of Cereal Science (1990), 12(2), 123-36
CODEN: JCSCDA; ISSN: 0733-5210
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Structural homologies between wheat (Triticum aestivum) gluten proteins
and proteins present in well-washed starch granules were examd. with a
panel of mouse monoclonal and mouse and rabbit polyclonal
antibodies, using immunoblotting, ELISA, and immunocytochem.
methods. Many antibodies raised against gluten protein
fractions cross-reacted with starch granule proteins (SGP), but often

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weakly. **Antibodies** with similar gliadin and glutenin subunit specificities had similar SGP specificities. **Antibodies** to high-mobility (.alpha.-, .beta.-, .gamma.-) gliadins cross-reacted weakly with low-mol.-wt. SGP (Mr 8000, 19,000 and 30,000) on immunoblots, and very weakly in indirect ELISAs. Some of these **antibodies** labeled both protein bodies and the periphery of starch granules in sections of immature grain, consistent with low-mol.-wt. SGP, deemed to be surface SGP on the basis of extractability studies, indeed being present on the granule surface. Monoclonal **antibodies** that bound .gamma.- or .omega.-gliadins and glutenin subunits bound to higher mol. wt. SGP, esp. a protein of Mr 77,000, at concns. only slightly above those which labeled gluten proteins. As the interior of the starch granule section was labeled, these proteins are likely to be integral to the granule. **Antibodies** binding broadly to all major gluten protein classes also bound most high and low-mol.-wt. SGPs. Some starch proteins of Mr 15,000, which have been assocd. with endosperm softness, appeared to be immunol. distinct.

L9 ANSWER 31 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:629824 CAPLUS

DOCUMENT NUMBER: 113:229824

TITLE: Wheat low-molecular-weight glutenin subunits - structural relationship to other gluten proteins analyzed using specific **antibodies**

AUTHOR(S): Skerriitt, John H.; Robson, Lisa G.

CORPORATE SOURCE: Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1990), 67(3), 250-7

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The immunol. homol. of low-mol. wt. glutenin subunits (LMW-GS) were compared with the other major wheat gluten polypeptides, high-mol.-wt. glutenin subunits (HMW-GS), and gliadins. Conventional 1-dimensional polyacrylamide gel electrophoretic (PAGE) methods were used as well as a 2-step, 1-dimensional sodium dodecyl sulfate-page technique, together with immunoblotting and enzyme-immunoassay methods. Many **antibodies** raised to gliadins and HMW-GS bound well to LMW-GS. **Antibodies** with specificities for similar groups of gliadins bound to similar groups of glutenins; and HMW-GS but not to other grain proteins, suggesting the existence of "common gluten" amino acid sequences or conformations. The soly. and immunochem. similarities as well as the known linkage between the genes for LMW-GS and certain gliadins mean that LMW-GS may be responsible for many biochem. properties and quality effects usually attributed to gliadins.

L9 ANSWER 32 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:512017 CAPLUS

DOCUMENT NUMBER: 113:112017

TITLE: Cereal identification using **antibodies** to characteristic protein, and kits containing the **antibodies**

INVENTOR(S): Skerriitt, John Howawrd; Wrigley, Colin

Walter; Underwood, Patricia Anne

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, Australia

SOURCE: Pat. Specif. (Aust.), 12 pp.

CODEN: ALXXAP

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|------|----------|-----------------|----------|
| AU 592987 | B2 | 19900201 | AU 1986-57023 | 19850502 |
| AU 8657023 | A1 | 19861106 | | |

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PRIORITY APPLN. INFO.: AU 1985-401 19850502

AB A cereal variety or quality type is identified by applying a cereal grain ext. or grain germination product to a suitable support, treating the support with a (monoclonal) antibody to a specific protein, and detg. the amt. of bound antibody. In an EIA for barley using antibodies to B- and C-hordeins, varieties more suitable for beer malting showed greater rates of destruction of antibody binding sites than poorer quality varieties. Assays using immobilized capture antibodies are also described.

L9 ANSWER 33 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:404802 CAPLUS

DOCUMENT NUMBER: 113:4802

TITLE: Homologies between grain storage proteins of different cereal species. 2. Effects of assay format and grain extractant on antibody cross-reactivity

AUTHOR(S): Skerriitt, John H.; Hill, Amanda S.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Cereal Science (1990), 11(2), 123-41

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A variety of monoclonal antibodies with specificities for different wheat grain storage proteins has been shown to exhibit a no. of differing cross-reaction patterns with grain storage proteins from related cereal species (Skerrett and Lew, 1990). This antibody library provides an opportunity to measure the effects of a range of immunoassay methodol. variables on the cross-reactivity of these antibodies. Variation of the extractant used for grain proteins from different cereals altered both the amt. and compn. of protein extd. and thus the cross-reaction of the antibodies. Antibody cross-reactivity was greater when nitrocellulose membrane solid phases compared with polystyrene microwells were used for indirect ELISA. Quite differing cross-reactivity results were obtained when the same grain protein exts. were used in indirect, antigen-competition and sandwich-type assay formats. In the sandwich assay format, alteration of either the solid phase-bound or labeled antibody altered apparent antibody specificity. Thus, it is important when reporting immunol. homol. data, to define cross-reaction of antibodies with respect to the assay format used. Antibody specificity (or cross-reactivity) can be manipulated by variation of sample extractant, solid phase and the format of the assay.

L9 ANSWER 34 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:404801 CAPLUS

DOCUMENT NUMBER: 113:4801

TITLE: Homologies between grain storage proteins of different cereal species. 1. Monoclonal antibody reaction with total protein extracts

AUTHOR(S): Skerriitt, John H.; Lew, Patricia Y.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Cereal Science (1990), 11(2), 103-21

CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The interactions of a library of monoclonal antibodies, prepd. to wheat (Triticum aestivus L.) gluten proteins, with exts. of total seed storage protein from a no. of related cereals was studied qual. using SDS-PAGE and immunoblotting techniques and studied quant. using indirect enzyme-immunoassay. Antibodies were of four cross-reaction types: (1) some antibodies, such as many of those binding .alpha.- and .beta.-gliadins, bound selectively to wheat grain proteins, (2) others with similar gliadin specificities, bound to prolamins from other Festucoid species (rye, barley and oats),

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(3) other **antibodies** specific for certain .gamma.- and .omega.-gliadins and high-mol.-wt. glutenins, bound very well to proteins from wheat, rye and barley grain, while (4) some **antibodies** showed anomalous cross-reactivities, binding well to wheat and maize prolamins but very weakly to rye or barley grain proteins. These homologies were generally in keeping with structural homologies of proteins from various cereal grains obtained from DNA sequencing and cross-hybridization studies. In some cases, new homologies were identified.

L9 ANSWER 35 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1990:156891 CAPLUS

DOCUMENT NUMBER: 112:156891

TITLE: **Antibody** responses reveal differences in oral tolerance to wheat and maize grain protein fractions

AUTHOR(S): Johnson, R. B.; Labrooy, J. T.; Skerritt, J. H.

CORPORATE SOURCE: Dep. Med., Univ. Adelaide, Adelaide, Australia

SOURCE: Clinical and Experimental Immunology (1990), 79(1), 135-40

CODEN: CEXIAL; ISSN: 0009-9104

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The influence of diet on humoral immune responses to gluten- and corn-derived proteins was examd. by ELISA and protein blotting techniques. Mice raised on the corn-based (gluten-free) diet responded well to parenteral immunization with each of 6 gluten-derived protein preps. (whole gliadin, 2 omega-gliadin fractions, wheat salt-sol. proteins, a peptic-tryptic digest, and a subtilisin digest of gluten); serum **antibody** levels increased at least 300-fold in each case. In contrast, mice raised on the wheat-based diet responded poorly to immunization with either whole gliadin or omega-gliadin and were virtually nonresponsive to enzymic digest of gluten. Diet had little effect on the magnitude of the **antibody** response to wheat salt-sol. proteins, with both groups showing a 300-fold increase in titer. Similarly, tolerance to .alpha.-zeins, the alc.-sol. proteins of corn did not occur on either diet. Some oral tolerance was obsd. to corn glutelin. The specificity of the various **antibody** responses was then analyzed by immunoblotting. Following immunization with gluten proteins or digests, **antibodies** from the corn-fed mice bound more or less equally to each of the main gliadin bands and to the glutenins, whereas the mice on the wheat-based diet had **antibody** specific for omega-gliadin proteins. Serum **antibodies** from the corn-fed mice, immunized with either .alpha.-zein or corn glutelin, showed even labeling of the major corn endosperm proteins whereas **antibodies** from mice on the wheat diet showed strong labeling of the mol. wt. 27,000 and 58,000 bands. Diet influenced the specificity, as well as the magnitude, of serum **antibody** responses to cereal proteins. In addn., oral tolerance appeared to affect the humoral response to some cereal proteins more than others. Both of these findings have important implications for the understanding of celiac disease.

L9 ANSWER 36 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:572723 CAPLUS

DOCUMENT NUMBER: 111:172723

TITLE: Detection of glutens with monoclonal **antibody** -producing hybridoma cells

INVENTOR(S): Skerritt, John Howard; Hill, Amanda Susanne

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, UK

SOURCE: Brit. UK Pat. Appl., 21 pp.

CODEN: BAXXDU

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

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PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|------|----------|-----------------|----------|
| GB 2207921 | A1 | 19890215 | GB 1988-16366 | 19880708 |
| GB 2207921 | B2 | 19910529 | | |
| AU 8818917 | A1 | 19890112 | AU 1988-18917 | 19880708 |
| AU 611921 | B2 | 19910627 | | |
| CA 1294903 | A1 | 19920128 | CA 1988-571492 | 19880708 |
| PRIORITY APPLN. INFO.: | | | AU 1987-2985 | 19870708 |

AB Hybridoma cell line ATCC HB9798 producing monoclonal antibodies (Mabs) against .omega.-gliadin of wheat and related proteins in rye and barley is prepd. The Mabs can be used for quant. and qual. detn. of gluten in samples. Balb/c mice were grown on a gluten-free diet till parturition and mated. After weaning, the female progeny were reared for one month on the gluten-free diet and immunized with .omega.-gliadin. Spleens were removed from mice and the cells were fused with mouse myeloma cell line sp 2/0. After selection, hybridoma 401/21 subclones were screened and further grown as ascites tumors to obtain antibody 401/21. The antibody 401/21 was immobilized on flat-bottom 96-well polystyrene microwell plates or strips for ELISA of food samples. The method could detect 0.01 and 0.001% (wt./wt.) gluten in food samples depending upon the diln. of the gluten ext.: lower levels were detectable in more concd. exts.

L9 ANSWER 37 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:491681 CAPLUS

DOCUMENT NUMBER: 111:91681

TITLE: Monoclonal antibodies used to characterize cDNA clones expressing specific wheat endosperm proteins

AUTHOR(S): Donovan, G. R.; Skerritt, J. H.; Castle, S. L.

CORPORATE SOURCE: Div. Plant Ind., CSIRO Wheat Res. Unit, North Ryde, Australia

SOURCE: Journal of Cereal Science (1989), 9(2), 97-111
CODEN: JCSCDA; ISSN: 0733-5210

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A wheat cDNA library, prepd. from grain endosperm poly A+ mRNA and cloned into the Escherichia coli expression vector lambda gt11, has been screened with 9 monoclonal antibodies having specificities for different wheat endosperm proteins. At least 1 pos. cDNA clone was isolated and purified from those selected with each antibody. Each purified cDNA clone was induced to express fusion proteins, and the nitrocellulose membranes to which the proteins were transferred were incubated with each of the other antibodies at .gtoreq.2 concns. to investigate the extent of homologies between expression fusion proteins. The specificities of the antibodies were detd. using immunoblotting under the same conditions used for binding to the fusion proteins from the expressed cDNA clones. Denatured DNA from each antibody-selected cDNA clone was also characterized by hybridization to .alpha.-/.beta.-genomic gliadin and genomic high-mol.-wt. glutenin subunit DNA probes. Northern hybridizations using the isolated cDNA as probes for endosperm mRNA were also used to assist clone identification. Some monoclonal antibodies with overlapping specificities (identified from blotting and ELISA expts.) crossreacted with several expressed cDNA clones. However, in other instances, pos. identifications were made of the proteins coded for by single families of the cDNA clones. Monoclonal antibody screening of a wheat cDNA library is useful in identifying families of cDNA clones corresponding to different wheat polypeptides at the primary screening stage, obviating the need in many instances for the application of more tedious methods of clone identification.

L9 ANSWER 38 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:230112 CAPLUS

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DOCUMENT NUMBER: 110:230112
 TITLE: Protein modification during malting and brewing: some new analytical methods
 AUTHOR(S): Skerritt, J. H.; Collings, D.
 CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, Australia
 SOURCE: Proceedings of the Convention - Institute of Brewing (Asia Pacific Section) (1988), 20th, 87-93
 CODEN: IBAZA2; ISSN: 0367-6897

DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Modern protein anal. methods, including size-exclusion and reversed-phase HPLC, PAGE, and monoclonal antibody tests were used to examine protein modification in grain during malting and in mash exts. and wort in brewing. Size-exclusion HPLC and electrophoresis are useful for providing qual. anal. of malt modification and proteolysis and protein pptn. during mashing; hydrolysis of specific proteins can also be quantified by HPLC or by immunoassay. Other antibody tests to measure residual protein from malt and cereal adjuncts in finished beers and to det. whether proteolytic enzymes were used in chillproofing of beers are also described.

L9 ANSWER 39 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:191088 CAPLUS

DOCUMENT NUMBER: 110:191088

TITLE: Monoclonal antibody specific to gliadin protein of wheat, its production and use in kits and methods for detection of gliadin in food

INVENTOR(S): Skerritt, John Howard; Wrigley, Colin
 Walter; Underwood, Patricia Anne

PATENT ASSIGNEE(S): Commonwealth Scientific and Industrial Research Organization, Australia

SOURCE: Pat. Specif. (Aust.), 16 pp.

CODEN: ALXXAP

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------|------|----------|-----------------|----------|
| AU 572955 | B2 | 19880519 | AU 1985-38501 | 19840206 |
| AU 8538501 | A1 | 19850815 | | |

PRIORITY APPLN. INFO.: AU 1984-3475 19840206

AB A hybridoma is manufd. which produces antibody specific for heat-stable and low-mobility gliadin(s). The antibody is used in a kit and immunoassay method for detecting gliadin in food. Mice were immunized with purified bread wheat gliadin and the spleen cells were fused with mouse myeloma Sp2/0 using PEG. The resultant hybrid cells were cloned and screened with wheat grain proteins. Of 386 clones examd., 2 secreted antibodies interacting with certain discrete bands in the .gamma.- and .omega.-gliadin regions of gradient gel electrophoresis-sepd. proteins. Neither rye pollen proteins nor a variety of other proteins (bovine milk .alpha.-lactalbumin, soybean trypsin inhibitor, etc.) bound these antibodies.

L9 ANSWER 40 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1988:525977 CAPLUS

DOCUMENT NUMBER: 109:125977

TITLE: Accumulation of gliadin and glutenin polypeptides during development of normal and sulfur-deficient wheat seed: analysis using specific monoclonal antibodies

AUTHOR(S): Skerritt, J. H.; Lew, P. Y.; Castle, S. L.

CORPORATE SOURCE: Div. Plant Ind., CSIRO, North Ryde, 2113, Australia

SOURCE: Journal of Experimental Botany (1988), 39(203), 723-37

CODEN: JEBOA6; ISSN: 0022-0957

DOCUMENT TYPE: Journal

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LANGUAGE: English

AB A panel of monoclonal **antibodies** with various specificities for wheat (*Triticum aestivum*) gluten polypeptides has been used to analyze the accumulation of these polypeptides in the endosperm of developing wheat seeds grown under normal and S-deficient conditions. Immunoblots of polypeptides fractionated by SDS-PAGE allowed a qual. anal. of gliadin and high-mol.-wt. (HMW) glutenin accumulation for high- and low-S seeds 8-30 days after anthesis (d.a.a.). In addn., quant. anal. of the deposition of various gluten polypeptides was performed, with a solid-phase RIA on exts. of seeds harvested 4-36 d.a.a. The initial accumulation of HMW glutenin subunits was detectable at an earlier stage of development than that of gliadins for both normal and S-deficient seeds. The initiation of detectable gliadin accumulation was asynchronous with an order of .alpha.-gliadins, .beta.-, .gamma.- and some .omega.-gliadins and finally the remaining .omega.-gliadins. In S deficiency, all gliadins reached a const. proportion of the dry wt. of the endosperm earlier than in normal wheat, while a more marked increase in the proportion of HMW glutenin occurred late in grain development. The protein blot studies also identified a putative .omega.-gliadin polypeptide which was detectable late in seed development and only in S-deficient seeds.

L9 ANSWER 41 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:194871 CAPLUS

DOCUMENT NUMBER: 106:194871

TITLE: Monoclonal **antibodies** in agricultural testing: quantitation of specific wheat gliadins affected by sulfur deficiency

AUTHOR(S): Skerriitt, John H.; Martinuzzi, Ornella; Wrigley, Colin W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
SOURCE: Canadian Journal of Plant Science (1987), 67(1), 121-9
CODEN: CPLSAY; ISSN: 0008-4220

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Proteins correlation with end-use quality in wheat (*Triticum aestivum* L.) flour samples have been quantitated using a panel of monoclonal **antibodies** (MCA) with specificities for different gliadins (grain endosperm storage proteins which are sol. in aq. alc.). A beta-gliadin specific **antibody** was found suitable for measuring sulfur-related quality loss in sets of flours from three wheat cultivars grown under varying conditions of sulfur fertilization. Binding of this monoclonal **antibody**, measured in a competitive enzyme-immunoassay, was highly correlated with flour sulfur and with the extensibility of, and resistance to stretching of doughs prepd. from these flour samples. These results demonstrate that monoclonal **antibodies** may be used to measure levels of specific components which vary as the technol. quality of the food varies. Rapid spot-tests based on the reaction of seed proteins with specific monoclonal **antibodies** may aid progeny selection in plant breeding program.

L9 ANSWER 42 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:135178 CAPLUS

DOCUMENT NUMBER: 106:135178

TITLE: Distinction between barley varieties by grain characteristics, electrophoresis, chromatography and **antibody** reaction

AUTHOR(S): Burbidge, M. J.; Batey, I. L.; Campbell, W. P.; Skerriitt, J. H.; Wrigley, C. W.

CORPORATE SOURCE: Rohstoffabt., VLB, Berlin, D-1000/65, Fed. Rep. Ger.
SOURCE: Seed Science and Technology (1986), 14(3), 619-29
CODEN: SSTCBK; ISSN: 0251-0952

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review and discussion with 10 refs. of methods of identification of barley varieties, e.g., visual examn., gel electrophoresis, HPLC, and immunol.

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L9 ANSWER 43 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:115996 CAPLUS

DOCUMENT NUMBER: 106:115996

TITLE: Improved staining and characterization of proteins

following gel electrophoresis and electroblotting

Wrigley, Colin W.; Skerritt, John H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE: Electrophor. '86 [Eighty-Six], Proc. Meet. Int.

Electrophor. Soc., 5th (1986), 291-303. Editor(s):

Dunn, Michael J. VCH: Weinheim, Fed. Rep. Ger.

CODEN: 55IZAB

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Improvements in immunol. techniques for characterizing protein zones after gel electrophoresis and electrophoretic transfer to nitrocellulose are illustrated, using wheat grain proteins as antigens and monoclonal or serum antibodies. Techniques included alkali enhancement of protein staining and immunol. reactivity of electroblotted proteins, avoidance of nonspecific antibody binding, and preparative use of electroblotting for protein purifn.

L9 ANSWER 44 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1987:48365 CAPLUS

DOCUMENT NUMBER: 106:48365

TITLE: Specificity characteristics of monoclonal

antibodies to wheat grain storage

proteins

AUTHOR(S): Skerritt, John H.; Underwood, P. Anne

CORPORATE SOURCE: Div. Mol. Biol., CSIRO, North Ryde, 2113, Australia

SOURCE: Biochimica et Biophysica Acta (1986), 874(3), 245-54

CODEN: BBACAQ; ISSN: 0006-3002

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A variety of monoclonal antibodies was prepd. to wheat (Triticum aestivum) gluten proteins, and their antigenic specificities were assessed using non-denaturing polyacrylamide gradient and SDS-PAGE and immunoblotting techniques. While most anti-gliadin monoclonal antibodies bound to all gliadin protein bands sepd. by 1-dimensional electrophoresis, several antibodies binding to small groups of gliadin proteins were identified. At high concns., these specific antibodies bound to an increasing no. of gliadins; this is likely due to the very high sequence homologies between groups of gliadin proteins. Several monoclonal antibodies with specificities for glutenin proteins were produced. These antibodies bound to all major glutenin subunits, although at low antibody concns. some bound selectively to a single subunit. Other anti-glutenin antibodies bound to minor glutenin subunits and a variety of gliadin proteins. Several bound to .gamma.-gliadins and high-mol.-wt. glutenins, suggesting that these groups of proteins bear considerable homol. The results are reviewed in relation to known information on gluten protein structure, derived from DNA-sequencing studies.

L9 ANSWER 45 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:624490 CAPLUS

DOCUMENT NUMBER: 105:224490

TITLE: New approaches to barley variety identification and quality studies

AUTHOR(S): Skerritt, J. H.; Batey, I. L.; Wrigley, C.

W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, Australia

SOURCE: Proceedings of the Convention - Institute of Brewing

(Asia Pacific Section) (1986), 19th, 55-62

CODEN: IBAZA2; ISSN: 0367-6897

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Three new approaches, which rely on differences in hordein compn. or

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properties, were investigated for their suitability as barley variety identification methods, to supplement visual and electrophoretic methods. High-performance liq. chromatog. on either ion-exchange or reversed-phase columns can differentiate barley varieties that cannot be distinguished by electrophoresis. Differences in the interaction of hordeins from various varieties with a set of monoclonal antibodies may form the basis for rapid spot-test for confirmation of variety or quality type. In addn., a very simple test based upon differences in the turbidity of grain exts. will be of use in preliminary screening of barley samples. There is potential for these new methods to be applied to malt anal.: both varietal identification of malts and detn. of the extent of (protein) modification. Components yielding processing problems can be identified and quantitated in malt samples.

L9 ANSWER 46 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:570903 CAPLUS

DOCUMENT NUMBER: 105:170903

TITLE: Molecular comparison of alcohol-soluble wheat and buckwheat proteins

AUTHOR(S): Skerritt, J. H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia

SOURCE: Cereal Chemistry (1986), 63(4), 365-9

CODEN: CECHAF; ISSN: 0009-0352

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Comparisons of buckwheat and wheat proteins according to amino acid compn., electrophoresis, and immunol. reaction revealed little or no similarities. Whereas most of the material extd. from wheat flour by 70% EtOH (following salt extn.) was protein in nature, similar exts. from buckwheat contained only 2.4% N. Unlike wheat gliadin, the corresponding buckwheat fraction was rich in lysine, arginine, and glycine; it was not electrophoretically resolvable into gliadinlike bands on lactate-buffered polyacrylamide gels, and on SDS polyacrylamide gels; it had only minor components in the gliadin mol. size range. Immunol. studies with rabbit polyclonal and mouse monoclonal antibodies showed little cross-reactivity between cereal prolamins and buckwheat proteins. Celiac sera with high IgG anti-gliadin titers also reacted very weakly with buckwheat proteins. These results suggest that alc.-sol. buckwheat proteins (which are only minor components of the endosperm) bear little mol. similarity to wheat prolamins; descriptions of the former as glutenlike are misleading.

L9 ANSWER 47 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49930 CAPLUS

DOCUMENT NUMBER: 104:49930

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: choice of primary and secondary antibodies

AUTHOR(S): Skerritt, John H.; Diment, John A.; Wrigley, Colin W.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 995-1003

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Of a series of monoclonal antibodies prepd. to cereal proteins, 2 antibodies with specificity for low-mobility, heat-stable prolamins in wheat and related cereals were investigated as possible probes for a test for gluten in cooked or processed foods. Urea-based solvents were superior to iso-PrOH or SDS extractants in allowing sensitive detection of trace amts. of prolamins. The antibodies detected bread and durum wheat and rye prolamins most strongly, followed by barley then oats; detection of corn and rice was quite weak. This selectivity is suitable for a test for prolamins toxic to coeliac-disease patients. Several enzyme-labeled 2nd

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antibodies, for detection of monoclonal antibody bound to cereal protein, were unsuitable reagents since an appreciable fraction of the 2nd antibodies bound directly to the cereal proteins. Sensitive, artifact-free detection of antibody binding could be performed using the peroxidase-antiperoxidase technique or by direct conjugation of horseradish peroxidase to the monoclonal antibodies.

L9 ANSWER 48 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49929 CAPLUS

DOCUMENT NUMBER: 104:49929

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: quantitative immunoassay

AUTHOR(S): Skerritt, John H.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 987-94

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An enzyme-coupled monoclonal antibody has been used to quantify gliadin-like immunoreactivity in a variety of foods. Small discs of nitrocellulose are soaked in food ext. or a series of std. gliadin solns., and incubated with antibody and an enzyme substrate yielding a sol. product. By use of a photometer, std. curves for gliadin may be constructed and the apparent gliadin content of samples calcd. The reproducibility of the procedure was examd. using a variety of common foods and food proteins. The limit of detection for wheat gliadin was .apprx.20 .mu.g/mL ext.; gliadin levels in excess of this value were found in some gluten-free bread mixes and starch [9005-25-8] sources. The overall time for anal. is 5-6 h, although for large nos. of samples, overnight blocking of non-specific antibody binding may be used. It is possible that a library of enzyme-linked monoclonal antibodies could be developed as useful tools for specific food anal.

L9 ANSWER 49 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:49928 CAPLUS

DOCUMENT NUMBER: 104:49928

TITLE: A sensitive monoclonal-antibody-based test for gluten detection: studies with cooked or processed foods

AUTHOR(S): Skerritt, John H.; Smith, Robyn A.

CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, NSW 2113, Australia

SOURCE: Journal of the Science of Food and Agriculture (1985), 36(10), 980-6

CODEN: JSFAAE; ISSN: 0022-5142

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A method for detection of wheat, rye, barley and oat proteins in a wide range of foods, including baked goods and processed meats has been developed. The procedure requires immobilization of food exts. on nitrocellulose paper followed by treatment with an enzyme-conjugated monoclonal antibody. Upon addn. of the appropriate enzyme substrate, gluten-contg. foods yield purple spots; a wide range of non-gluten common food proteins did not react. The method has several advantages over other means of detecting cereal protein, such as electrophoresis. It is rapid, requiring little sample prepn., and does not require sophisticated equipment or prior knowledge of electrophoretic patterns of common non-cereal food proteins. Since the method may be used with cooked or baked foods, it should be suitable for food-monitoring applications.

L9 ANSWER 50 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:33153 CAPLUS

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DOCUMENT NUMBER: 104:33153
 TITLE: Detection and quantitation of cereal protein in foods using specific enzyme-linked monoclonal antibodies
 AUTHOR(S): Skerriitt, John H.
 CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
 SOURCE: Food Technology in Australia (1985), 37(12), 570-2
 CODEN: FTAUAC; ISSN: 0015-6647
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A simple test for the presence and level of cereal gluten proteins in foods has been developed using monoclonal antibodies with specificity for heat-stable proteins from wheat, rye, barley, and oat grain. The test is faster, more sensitive and more reliable than other methods, such as electrophoresis, and may be applied to both cooked or processed as well as raw foods. The ability of monoclonal antibodies to act as sensitive reagents having reproducible specificities should allow their use in a wide range of immunochem. methods in food anal.

L9 ANSWER 51 OF 51 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 1985:59452 CAPLUS
 DOCUMENT NUMBER: 102:59452
 TITLE: Monoclonal antibodies to gliadin proteins used to examine cereal grain protein homologies
 AUTHOR(S): Skerriitt, John H.; Smith, Robyn A.; Wrigley, Colin W.; Underwood, P. Anne
 CORPORATE SOURCE: Wheat Res. Unit, CSIRO, North Ryde, 2113, Australia
 SOURCE: Journal of Cereal Science (1984), 2(4), 215-24
 CODEN: JCSCDA; ISSN: 0733-5210
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB Monoclonal antibodies were prepd. to a gliadin protein ext. of bread wheat (Triticum aestivum cv Timgalen) and specific antibody-cereal protein interactions were detected using horseradish peroxidase-coupled second antibodies after transfer of proteins to nitrocellulose following electrophoresis. Whereas some antibodies had broad specificity for gliadin protein, other antibodies of narrower specificity were investigated further. The latter antibodies were selective for omega-gliadins and bound neither high-mol.-wt. glutenin subunits albumin and globulin wheat proteins, nor a wide variety of other proteins. However, certain related cereal species such as durum wheat, barley, and rye contained endosperm proteins recognized by these monoclonal antibodies. This observation confirms that sequence homologies exist between prolamins from wheat and related cereal species as well as between certain gliadins from hexaploid wheat.

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L16 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS on STN
 ACCESSION NUMBER: 2000:335649 CAPLUS
 DOCUMENT NUMBER: 132:333681
 TITLE: Detection of preharvest sprouting in cereal grains by immunoassay of .alpha.-amylase
 INVENTOR(S): Skerritt, John Howard
 PATENT ASSIGNEE(S): Quality Wheat CRC Limited, Australia
 SOURCE: PCT Int. Appl., 51 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|-----------------|----------|
| WO 2000028319 | A1 | 20000518 | WO 1999-AU995 | 19991111 |
| W: AU, CA, JP, US | | | | |
| RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| CA 2345403 | AA | 20000518 | CA 1999-2345403 | 19991111 |
| EP 1137935 | A1 | 20011004 | EP 1999-957719 | 19991111 |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI | | | | |
| JP 2002529735 | T2 | 20020910 | JP 2000-581446 | 19991111 |
| AU 757926 | B2 | 20030313 | AU 2000-15341 | 19991111 |
| PRIORITY APPLN. INFO.: AU 1998-7058 A 19981111 | | | | |
| WO 1999-AU995 W 19991111 | | | | |

AB A two-site immunoassay for the qual. or quant. detection of .alpha.-amylase in a test sample comprises: (i) exposing the test sample to a first ("capture") antibody or antibody fragment which specifically or preferentially binds to a first epitope on the .alpha.-amylase under conditions permitting binding; (ii) subsequently exposing bound .alpha.-amylase to a second ("detection") antibody or antibody fragment which specifically or preferentially binds to a second epitope on the .alpha.-amylase that is distinct from the first epitope, under conditions permitting binding of the second antibody or its fragment to the bound .alpha.-amylase; and (iii) detecting any binding of the second antibody or its fragment to the bound .alpha.-amylase, wherein either of the first or second epitopes is an epitope comprising one or more of the amino acid sequences: IDRLVSIRTRGQIHS, CRDDRPYADG, or VNWNKVGGS and variants thereof showing .gtoreq.80% (preferably .gtoreq.90%) sequence identity. The immunoassay is useful for detecting weather damage (i.e., preharvest sprouting) in cereal grain. Thus, a rapid tube sandwich ELISA detected .alpha.-amylase in preharvest-sprouted wheat exts. at .apprx.4 ng/mL.

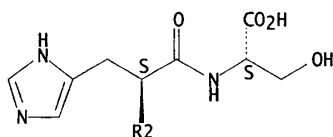
IT 268202-94-4 268202-95-5 268202-96-6
 RL: ANT (Analyte); ANST (Analytical study)
 (detection of preharvest sprouting in cereal grains by immunoassay of .alpha.-amylase)

RN 268202-94-4 CAPLUS

CN L-Serine, L-isoleucyl-L-.alpha.-aspartyl-L-alanyl-L-leucyl-L-valyl-L-seryl-L-isoleucyl-L-arginyl-L-threonyl-L-arginylglycyl-L-glutamyl-L-isoleucyl-L-histidyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

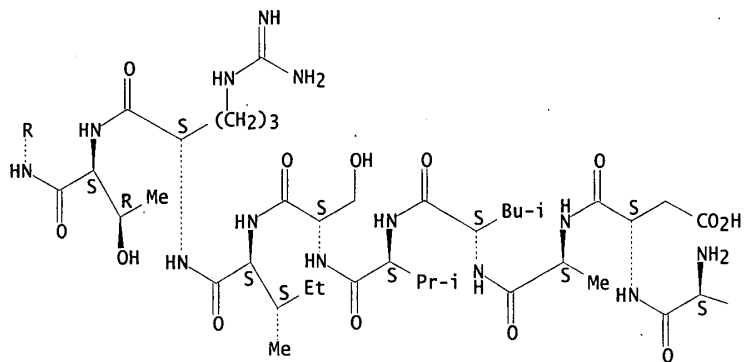


Searched by Susan Hanley 305-4053

Page 1

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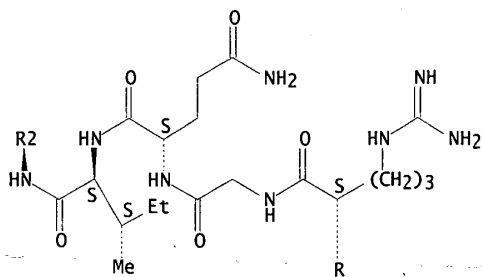
PAGE 2-A



PAGE 2-B



PAGE 3-A

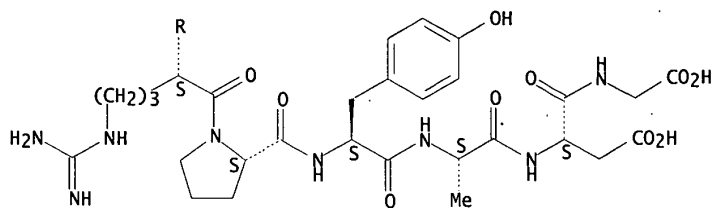


RN 268202-95-5 CAPLUS
 CN Glycine, L-cysteinyl-L-arginyl-L-.alpha.-aspartyl-L-.alpha.-aspartyl-L-
 arginyl-L-prolyl-L-tyrosyl-L-alanyl-L-.alpha.-aspartyl- (9CI) (CA INDEX
 NAME)

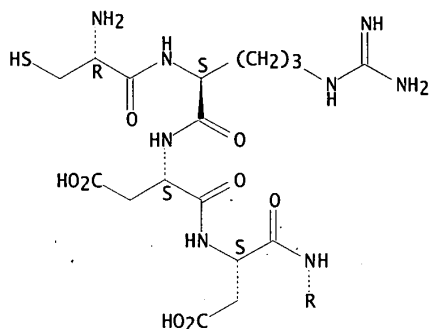
Absolute stereochemistry.

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PAGE 1-A



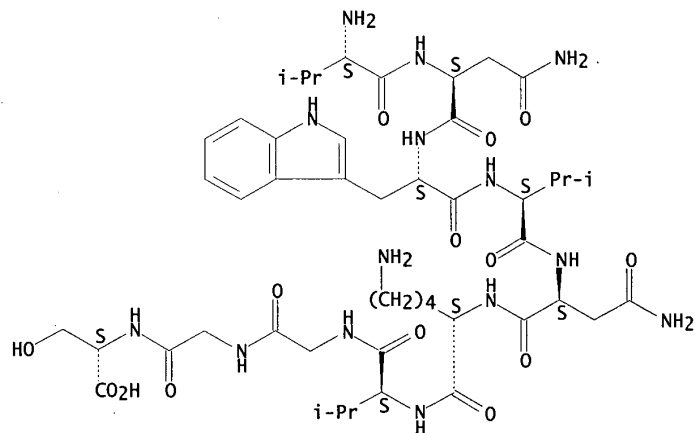
PAGE 2-A



RN 268202-96-6 CAPLUS

CN L-Serine, L-valyl-L-asparaginy1-L-tryptophyl-L-valyl-L-asparaginy1-L-lysy1-L-valylglycylglycyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



REFERENCE COUNT:

3

THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:35:10 ; Search time 45.8571 Seconds

(Without alignments)
51.920 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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| 6 | 45 | 61.6 | 429 | 16 | AAAR76520 |
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| 9 | 45 | 61.6 | 434 | 18 | AAAB10469 |

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| 11 | 45 | 61.6 | 434 | 20 | AAAB1375 | O. sativa alpha-am |
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| 17 | 42 | 57.5 | 168 | 21 | AAAB10643 | Human VEGF-x CUB-1 |
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| 72 | 40 | 54.8 | 130 | 23 | AAAB16273 | Human VEGF-x prote |
| 73 | 39 | 53.4 | 272 | 23 | AAAB92198 | Human VEGF-x prote |
| 74 | 39 | 53.4 | 293 | 24 | AAAB60037 | Human VEGF-x prote |
| 75 | 39 | 53.4 | 364 | 17 | AAAB96235 | Human VEGF-x prote |
| 76 | 39 | 53.4 | 417 | 21 | AAAB28529 | Human VEGF-x prote |
| 77 | 39 | 53.4 | 433 | 17 | AAAB88454 | Human VEGF-x prote |
| 78 | 39 | 53.4 | 440 | 14 | AAAR33744 | Human VEGF-x prote |
| 79 | 39 | 53.4 | 443 | 16 | AAAR74739 | Human VEGF-x prote |
| 80 | 39 | 53.4 | 443 | 16 | AAAR74739 | Human VEGF-x prote |
| 81 | 39 | 53.4 | 443 | 16 | AAAR74739 | Human VEGF-x prote |
| 82 | 39 | 53.4 | 445 | 21 | AAV32374 | Human VEGF-x prote |

| | | |
|--------------------------|---|--------------------------------------|
| AAAB12798 | ID | AAAB12798 standard; Protein; 428 AA. |
| XX | | |
| AC | | |
| XX | | |
| XX | AAAB12798; | |
| DT | 23-NOV-2000 | (first entry) |
| DE | Rice alpha-Amy7-C protein SEQ ID NO:2. | |
| XX | | |
| KW | Rice: alpha-Amy6-C; alpha-Amy7-C; alpha-Amy8-C; alpha-Amy10-C; | |
| KM | gene expression; promoter region; alpha-amylase; transgenic plant. | |
| XX | | |
| OS | Oryza sativa. | |
| PN | JP2000157080-A. | |
| PD | 13-JUN-2000. | |
| XX | | |
| PE | 04-NOV-1993; 99JP-0356560. | |
| PR | 05-NOV-1992; 92JP-0321274. | |
| PR | 04-NOV-1993; 93JP-0297607. | |
| XX | | |
| PA | (NASC-) NAT SCI COUNCIL. | |
| DR | WPI; 2000-468171/41. | |
| DR | N-PSDB; AAA72947. | |
| XX | | |
| PT | A gene expression system containing the promoter region of | |
| PT | alpha-amylase gene, useful for mass production of a desired gene | |
| PT | product in a plant host cell | |
| XX | | |
| PS | Example 1; Page 27-30; 39pp; Japanese. | |
| CC | XX | |
| CC | The present invention describes a gene expression system containing the | |
| CC | promoter region of an alpha-amylase gene. Also described is a method for | |
| CC | preparing a transgenic rice plant comprising: (1) infecting Agrobacterium | |
| CC | into an unmutated embryo of a rice plant; (2) simultaneously culturing | |
| CC | the embryo with a suspended culture of a dicotyledon during the | |
| CC | transforming step; (3) growing the transformed embryo to a callus in a | |
| CC | selective medium containing a plant growth hormone; and (4) regenerating | |
| CC | the callus to roots and sprouts in a regeneration medium. The method can | |
| CC | be used for mass production of a desired gene product in a plant host | |
| CC | cell. The present sequence represents the rice alpha-Amy7-C protein, | |
| XX | which is used in an example from the present invention. | |
| SQ | Sequence 428 AA: | |
| Query Match | 61.6%; Score 45; DB 21; Length 428; | |
| Best Local Similarity | 71.4%; Pred. No. 5; | |
| Matches 10; Conservative | 1; Mismatches 3; Indels 0; Gaps 0; | |
| OY | 1 IDRIVSIRTCGIH 14 : : | |
| bB | 359 IERLVSIRNRGSIH 372 | |
| RESULT 4 | | |
| ID | AAAM50251 | |
| XX | AAAM50251 standard; Protein; 428 AA. | |
| AC | AAAM50251; | |
| DT | 21-JAN-2002 | (first entry) |
| DE | Rice alpha-amylase (alpha-Amy7-C gene product). | |
| KW | Alpha-amylase; promoter; rice; transgenic plant; angiosperm; | |
| KM | monocot; cereal; brewing. | |
| XX | | |
| OS | Oryza sativa. | |
| PH | Key Location/Qualifiers | |

[illegible]

```

XX XX TW402638-A.
PN XX
XX XX 21-AUG-2000.
PD XX
XX XX 13-FEB-1992; 97TW-0101436.
PE XX
XX XX 13-FEB-1992; 97TW-0101436.
PR XX
XX XX 13-FEB-1992; 97TW-0101436.
PA XX
XX XX (NASC-) NAT SCI COUNCIL.
PI XX
XX XX Yu S, Liou L;
DR XX WPI; 2001-167365/17.
DR N-PSDB; AAH20283.
XX XX
XX XX Gene expression system comprising the promoter region of alpha-amylase
PT gene, produces large quantities of alpha-amylase in culture medium of
PT sugar starved rice -
XX XX
XX PS Disclosure; Fig 8; 104pp; Chinese.
XX XX
XX CC This invention relates to a gene expression system comprising the
CC alpha-amylase gene promoter. DNA encoding the signal peptide of
CC alpha-amylase and the promoter along with the glucuronidase reporter gene
CC and hygromycin resistance gene are used in the construction of a GUS gene
CC expression vector, which when transformed into rice suspension-cultured
CC cells, can be used to investigate the expression of the vector under the
CC control of the promoter. The gene expression system can be used to
CC conduct gene regulation and protein expression and secretion using the
CC characteristics of the alpha-amylase gene promoter and the DNA sequence
CC encoding the signal peptide. The present sequence represents an
CC alpha-amylase related protein used in the course of the present
CC invention.
XX XX
XX SQ Sequence 428 AA;
OY Query Match 61.6%; Score 45; DB 22; Length 428;
Best Local Similarity 71.4%; Pred. NO. 5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 IDRLVSTRGQIH 14
|:||||| | ||
DB 359 IERLVSTRGQIH 372
RESULT 6
AAR76520
ID AAR76520 standard; Protein: 429 AA.
XX AC
XX AC AAR76520;
XX DT 14-FEB-1996 (first entry) -
XX XX
XX DE Alpha-amylase-7-C.
XX XX
XX KW Alpha-Amy-6-C; amylase; promoter; vector; heterologous;
XX KW gene expression system.
XX OS
XX OS Oryza sativa.
XX XX
XX FH Key Location/Qualifiers
FT Misc-difference 35
FT /note= "corresp. to GAC codon"
FT Misc-difference 83
FT /note= "corresp. to CAG codon"
FT Misc-difference 158
FT /note= "corresp. to GAC codon"
FT Misc-difference 218
FT /note= "corresp. to TAC codon"
FT Misc-difference 224
FT /note= "corresp. to CGG codon"
FT Misc-difference 233

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FT FT /note= "corresp. to CGT codon"
FT Misc-difference 294
FT /note= "corresp. to CAG codon"
XX XX
XX XX JP07143895-A.
XX XX
XX XX 06-JUN-1995.
XX XX
XX XX 04-NOV-1993; 93JP-0297607.
XX XX
XX PR 05-NOV-1992; 92JP-0321274.
XX XX
XX PA (NASC-) NAT SCI COUNCIL.
XX XX
XX XX WPI; 1995-236472/31.
DR N-PSDB; AAQ92806.
XX XX
XX XX Gene expression system contg. alpha-amylase gene promoter - for use
PT in plants for expression of heterologous genes
PT XX
XX XX Claim 3; Page 27-30; 42pp; Japanese.
XX XX
XX PS AAR76519-R76521 represent the amylase gene products alpha-amylase-6-C,
XX CC alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter
XX CC regions of these amylase genes are used in a new gene expression system.
XX CC The system may be used for the expression of heterologous genes in plant
XX CC cells and for the large scale production of the encoded products of such
XX CC genes.
XX CC NI. some amino acids in this sequence appear to have been wrongly
XX CC entered, see feature table and the corresp. DNA file AAQ92806.
XX XX
XX SQ Sequence 429 AA;
OY Query Match 61.6%; Score 45; DB 16; Length 429;
Best Local Similarity 71.4%; Pred. NO. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 IDRLVSTRGQIH 14
|:||||| | ||
DB 360 IERLVSTRGQIH 373
RESULT 7
AAR55130
ID AAR55130 standard; Protein: 433 AA.
XX AC
XX AC AAR55130;
XX DT 25-MAR-2003 (updated)
XX DT 12-JAN-1995 (first entry)
XX XX
XX DE Rice alpha-amylase coding.
XX XX
XX KW Virus; recombination; plant virus; alpha trichosanthin; phenotype;
XX KW alpha amylase; alpha haemoglobin; bromo mosaic virus; gemini virus;
XX KW rice necrosis virus tobamovirus; gene expression; chinese cucumber.
XX OS
XX OS Oryza sativa.
XX XX
XX PN US5316931-A.
XX XX
XX PD 31-MAY-1994.
XX XX
XX XX 31-JUL-1992; 92US-0923692.
XX PF
XX PF 26-FEB-1988; 88US-0160766.
XX PR 26-FEB-1988; 88US-0160771.
XX PR 15-JUL-1988; 88US-0219279.
XX PR 17-FEB-1989; 89US-0310881.
XX PR 05-MAY-1989; 89US-0347637.
XX PR 08-JUN-1989; 89US-0363138.
XX PR 22-OCT-1990; 90US-0600244.
XX PR 16-JAN-1991; 91US-0641617.

```


CC replication, encapsidation and systemic spread in infected tobacco
CC plants, and directs expression of the alpha-amylase in plant
CC tissue.

XX Sequence 434 AA;

Query Match 61.6%; Score 45; DB 18; Length 434;
Best Local Similarity 71.4%; Pred. No. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIH 14
|:||||| | | | |
Db 365 IERLVSIRNRGOIH 378

RESULT 10
AAW1871
ID AAW1871 standard; Protein: 434 AA.

XX AAW1871;

DT 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)

XX Rice alpha-amylase.

KW Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KW alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
KW subgenomic promoter; coat protein.

OS Oryza sativa.

PN US589367-A.

XX 31-DEC-1996.

PD 19-JAN-1994; 94US-0184237.

XX 17-FEB-1989; 89US-0310881.

PR 05-MAY-1989; 89US-0347637.

PR 08-JUN-1989; 89US-0363138.

PR 31-JUL-1992; 92US-0923692.

PR 26-FEB-1988; 88US-0160766.

PR 15-JUL-1988; 88US-0160771.

PR 15-JUL-1988; 88US-0219279.

PR 22-OCT-1990; 90US-0600244.

PR 16-JAN-1991; 91US-0641617.

PR 26-JUL-1991; 91US-0737899.

PR 01-AUG-1991; 91US-0739143.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

PA Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

PI Turpen AM, Turpen TH;

XX WPI: 1997-076845/07.

DR N-PSDB: AAT61377.

XX Recombinant viral DNA for altering plant phenotype or protein prodn

PT - contains non-native sub-genomic promoter for expression of

PT heterologous protein and native promoter for expression of coat

PT protein

XX Example 4; Column 49-52; 42pp; English.

CC involving germ cell. The recombinant viruses are stable and can

CC cause systemic infection, with stable expression/transcription in

CC plants that are hosts for the non-native part of the vector. The

CC nucleotide sequences encoding these protein preferably integrated

CC in plant viruses having either the O-coat protein or the U1-coat

CC protein gene.

CC (Updated on 25-MAR-2003 to correct PF field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 434 AA;

Query Match 61.6%; Score 45; DB 18; Length 434;
Best Local Similarity 71.4%; Pred. No. 5.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIH 14
|:||||| | | | |
Db 365 IERLVSIRNRGOIH 378

RESULT 11
AAV01375
ID AAV01375 standard; Protein: 434 AA.

XX AAV01375;

DT 20-MAR-2003 (updated)

DT 04-JUN-1999 (first entry)

XX O. sativa alpha-amylase.

KW Recombinant; plant virus; coat protein; systemic infection;

KW transcription; therapeutic; rice; alpha-amylase.

OS Oryza sativa.

PN US5889190-A.

XX 30-MAR-1999.

PD 07-JUN-1995; 95US-0480432.

XX 17-FEB-1989; 89US-0310881.

PR 05-MAY-1989; 89US-0347637.

PR 08-JUN-1989; 89US-0363138.

PR 31-JUL-1992; 92US-0923692.

PR 19-JAN-1994; 94US-0184237.

PR 26-FEB-1988; 88US-0160766.

PR 15-JUL-1988; 88US-0219279.

PR 22-OCT-1990; 90US-0600244.

PR 16-JAN-1991; 91US-0641617.

PR 26-JUL-1991; 91US-0737899.

PR 01-AUG-1991; 91US-0739143.

XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.

PA Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;

PI Turpen AM, Turpen TH;

XX WPI: 1999-243290/20.

DR N-PSDB: AAX29144.

XX Recombinant plant viral nucleic acid derived from a plus sense,

PT single stranded RNA plant virus - useful for the transcription of

PT products in a host

XX Example 4; Columns 47-51; 46pp; English.

XX The invention relates to a recombinant plant viral nucleic acid derived

CC from a plus sense, single stranded RNA plant virus. The recombinant plant

CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter

CC that is native to the plus sense, single stranded RNA plant virus and

CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the
 CC first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic acid
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (Updated on 20-MAR-2003 to correct PR field.)

CC Sequence 434 AA;

Query Match 61.6%; Score 45; DB 20; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQIH 14
 |:||||||| | |
 DB 365 IERLVSIPTRGQIH 378

RESULT 12

AAW84383 standard; Protein: 434 AA.

AAW84383;

01-APR-1999 (first entry)

Rice alpha-amylase sequence.

Rice: alpha-amylase; plant virus: RNA plant virus promoter;

systemic infection; foreign gene expression; AIDS therapeutic drug.

Oryza sativa.

US5866785-A.

02-FEB-1999.

07-JUN-1995; 95US-0482920.

31-JUL-1992; 92US-0923692.

26-FEB-1988; 88US-0160766.

15-JUL-1988; 88US-0160771.

17-FEB-1988; 88US-0219279.

05-MAY-1989; 89US-0347637.

08-JUN-1989; 89US-0363138.

22-OCT-1990; 90US-0600244.

16-JAN-1991; 91US-0641617.

26-JUL-1991; 91US-0737899.

01-AUG-1991; 91US-0739143.

19-JAN-1994; 94US-0184237.

07-JUN-1995; 95US-0482920.

(BIOS-) BIOSOURCE TECHNOLOGIES INC.

Dawson WO, Turpen TJ, Garger SJ, Grantham GL, Grill LK;

WPI; 1999-142035/12.

N-PSDB; AAW03386.

Recombinant plant viral vector - that is capable of systemic

infection in host plant and stable production of heterologous DNA

useful for producing therapeutic proteins for treating e.g. AIDS

PS Example 4; Columns 51-54; 45pp; English.

XX The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the
 CC invention. The specification describes a recombinant plant viral
 CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
 CC a native (+)-sense RNA plant virus promoter that is linked to an
 CC expression sequence and a heterologous (+)-sense RNA plant virus
 CC promoter that is linked to an expression sequence. The promoters are
 CC incapable of recombination with each other, and one of the expression
 CC sequences encodes a plant viral coat protein while the other is
 CC optionally a heterologous coding sequence. The plant viral nucleic acid
 CC is capable of systemic infection in a host plant. The viral construct is
 CC useful for the introduction and expression of non-viral foreign genes
 CC in plants and the production of e.g. potential AIDS therapeutic drugs.

SO Sequence 434 AA;

Query Match 61.6%; Score 45; DB 20; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIPTRGQIH 14
 |:||||||| | |
 DB 365 IERLVSIPTRGQIH 378

RESULT 13

AAV87792 standard; Protein: 434 AA.

AAV87792;

24-AUG-2000 (first entry)

Rice alpha-amylase protein.

Animal RNA virus; viral coat protein; plant; male sterility;

interleukin; EPO; erythropoietin; CSF; colony stimulating factor;

Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;

Stereo specific catalysts; alpha-amylase; rice.

Oryza sativa.

US6054566-A.

25-APR-2000.

07-JUN-1995; 95US-0484341.

17-FEB-1989; 89US-0310881.

08-JUN-1989; 89US-0363138.

26-FEB-1988; 88US-0160766.

15-JUL-1988; 88US-0219279.

05-MAY-1989; 89US-0347637.

22-OCT-1990; 90US-0600244.

16-JAN-1991; 91US-0641617.

26-JUL-1991; 91US-0737899.

01-AUG-1991; 91US-0739143.

31-JUL-1992; 92US-0923692.

(BIOS-) BIOSOURCE TECHNOLOGIES INC.

Garger SJ, Grill LK, Turpen TJ, Grantham GL, Dawson WO, Turpen AW;

Donson J;

WPI; 2000-338510/29.

N-PSDB; AAV12394.

Recombinant non-retroviral nucleic acid for producing proteins such as

interleukins, melanin and vaccines, comprises subgenomic promoters

linked to sequences coding for viral coat protein and heterologous

PT proteins -
 XX
 PS Example 4; Column 65-68; 51pp; English.
 XX
 CC This invention describes a novel recombinant viral nucleic acid (1)
 CC from a non-retroviral (+) sense, single stranded animal RNA virus
 CC comprising a nucleic acid sequence coding for a viral coat protein
 CC regulated by a native subgenomic promoter and other two heterologous
 CC nucleic acid sequences regulated by two other subgenomic promoters.
 CC (1) is useful for expressing foreign genes e.g. genes inducing male
 CC sterility in plants. (1) is also useful for producing proteins such as
 CC interleukin, EPO (erythropoietin), CSF (colony stimulating factor),
 CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
 CC etc., and compounds that are useful for stereo specific catalysis of,
 CC organic compounds. (1) is stable and transcribed systematically. The dual
 CC subgenomic promoter system reduces the frequency of recombination thus
 CC reducing regeneration of the wild type virus. This sequence represents
 CC a rice alpha-amylase protein which is described in the method of the
 CC invention.
 XX
 SQ Sequence 434 AA;
 XX
 Query Match 61.6%; Score 45; DB 21; Length 434;
 Best Local Similarity 71.4%; Pred. No. 5.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1 IDRLVSIRTRGQIH 14
 I:|||||I I
 Db 365 IERLVSIRNRGSIH 378
 XX
 RESULT 14
 AAY35541
 ID AAY35541 standard; Protein; 460 AA.
 XX
 AC AAY35541;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE C. pneumoniae protein involved in intermediate metabolism.
 XX
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
 KW vaccine; neutralising epitope.
 XX
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB01890.
 XX
 PR 04-NOV-1998; 98US-0107078.
 PR 21-NOV-1997; 97FR-0014673.
 XX
 PA (GEST) GENSET.
 XX
 PI Griffais R;
 XX
 DR WPI: 1999-357842/30.
 XX
 PT Genome sequence of Chlamydia pneumoniae
 PS Page 1288-1289; Disclosure; 1912pp; English.
 PS
 XX AA34584-Y35879 represent the proteins encoded by all the open reading
 CC frames in the complete genome (see AA391990) of Chlamydia pneumoniae.
 CC C. pneumoniae causes respiratory disease such as pneumonia and
 CC bronchitis and is thought to be a contributing factor in heart
 CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AA34584-Y35879) can be used in

CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae.
 XX
 SQ Sequence 460 AA;
 XX
 Query Match 60.3%; Score 44; DB 20; Length 460;
 Best Local Similarity 57.1%; Pred. No. 8.5;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 2 DRLVSIRTRGQIHS 15
 |||:|:| |
 Db 407 DRLSMETGGLIHN 420
 XX
 RESULT 15
 AAU31870
 ID AAU31870 standard; Protein; 386 AA.
 XX
 AC AAU31870;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Novel human secreted protein #2361.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Dymnac RT;
 XX
 DR WPI: 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 521; 765pp; English.
 XX
 XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemia. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX
 SQ Sequence 386 AA;
 XX
 Query Match 58.9%; Score 43; DB 22; Length 386;

Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRLVSIRTRGQIHS 15
:111:111:11
DB 163 MDRLQLRSRNETHS 177

RESULT 16

AAAB10652
ID AAB10652 standard; Protein: 167 AA.

AAAB10652;

DT 19-JAN-2001 (first entry)

DE Human VEGF-X protein derived from clone 41.

KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antihemetic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

PN NO200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99MO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 990S-0124967.

PR 08-NOV-1999; 990S-0164131.

PA (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Goslowska A;

PI Dhanaraj SN, Xu J;

DR WPI: 2000-442669/38.

PS New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

PS Disclosure: Fig 12; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antihemetic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC derived from clone 41 which is described in the method of the invention.

XX Sequence 167 AA;

Query Match 57.5%; Score 42; DB 21; Length 167;

Best Local Similarity 42.9%; Pred. No. 6.4; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGQIHS 15
:111:111:11
DB 47 ERITVSTNGSIHS 60

RESULT 17

AAAB10643
ID AAB10643 standard; Protein: 168 AA.

AAAB10643;

DT 19-JAN-2001 (first entry)

DE Human VEGF-X CUB-like domain protein.

KW VEGF-X; vascular endothelial growth factor; human; vulnery; cytostatic;
KW antihemetic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.

OS Homo sapiens.

PN NO200037641-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99MO-US30503.

PR 22-DEC-1998; 98GB-0028377.

PR 18-MAR-1999; 990S-0124967.

PR 08-NOV-1999; 990S-0164131.

PA (JANC) JANSSEN PHARM NV.

PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JH, Goslowska A;

PI Dhanaraj SN, Xu J;

DR N-PSDB: AAA71987.

PS New vascular endothelial growth factor protein, useful for treating or

PT preventing diseases associated with inappropriate angiogenesis activity

PT such as cancer, rheumatoid arthritis, psoriasis and wounds -

PS Disclosure: Fig 26; 127pp; English.

CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnery, cytostatic, antihemetic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents a human VEGF-X protein
CC CUB-like domain which can be expressed in E. coli systems and which is
CC described in the method of the invention.

XX Sequence 168 AA;

Query Match 57.5%; Score 42; DB 21; Length 168;

Best Local Similarity 42.9%; Pred. No. 6.4; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGQIHS 15

```

Db          44 ERITVSTNGSIHS 57
          :|:::| | | |
RESULT 18
AAB10653
ID AAB10653 standard; Protein; 282 AA.
XX
AC AAB10653;
XX
DT 19-JAN-2001 (first entry)
DE Human VEGF-X protein derived from clone 20.
XX
XX VEGF-X; vascular endothelial growth factor; human; vulnery; cytosolic;
XX antihemetic; antiarthritic; antipsoriatic; antidiabetic; treatment;
XX angiogenesis regulator; vascularization regulator; cancer; psoriasis;
XX rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
XX tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
XX venous sore; diabetic ulcer; burns; skin graft growth.
XX
XX Homo sapiens.
XX
XX WO200037641-A2.
XX
XX 29-JUN-2000.
XX
XX 21-DEC-1999; 99WO-US30503.
XX
XX 22-DEC-1998; 98GB-0028377.
XX 18-MAR-1999; 99US-0124967.
XX 08-NOV-1999; 99US-0164131.
XX
XX (JANC ) JANSSEN PHARM NV.
XX
XX Gordon RD, Sprengel J, Yon JR, Dijkmans JTH, Gosiewska A;
XX Dhanaraj SN, Xu J;
XX
XX WPI; 2000-442669/38.
XX
XX New vascular endothelial growth factor protein, useful for treating or
XX preventing diseases associated with inappropriate angiogenesis actively
XX such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
XX Disclosure; Fig 12; 127pp; English.
XX
XX This invention describes a novel vascular endothelial growth factor-X
XX (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
XX vulnery, cytosolic, antihemetic, antiarthritic, antipsoriatic and
XX antidiabetic activity and acts as an angiogenesis and vascularization
XX regulator. An antisense molecule of the invention is useful for treating
XX or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
XX retinopathy by inhibiting angiogenic activity or inappropriate
XX vascularization including formation and proliferation of new blood
XX vessels, growth and development of tissues, tissue regeneration and organ
XX and tissue repair in a subject. The products of the invention are useful
XX for preparing medicaments for treating wounds such as dermal ulcers,
XX pressure sores, venous sores, diabetic ulcers and burns and to promote
XX skin graft growth, tissue repair, proliferation of new blood vessels,
XX tissue regeneration and organ repair by promoting angiogenic activity or
XX vascularization. This sequence represents the human VEGF-X protein
XX derived from clone 20 which is described in the method of the invention.
XX
XX Sequence 282 AA;
XX
XX Query Match 57.5%; Score 42; DB 21; Length 282;
XX Best Local Similarity 42.9%; Pred. No. 12;
XX Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 DRLVSIRTRGOIHS 15
XX :|:::| | | |
XX 47 ERITVSTNGSIHS 60
XX

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RESULT 19
AAY59286
ID AAY59286 standard; Protein; 297 AA.
XX
AC AAY59286;
XX
DT 25-APR-2000 (first entry)
DE Bone morphogenic protein (BMP) (clone HSYAE36).
XX
XX Bone morphogenic protein; BMP; cytosolic; osteopathic; angiogenic;
XX vulnery; bone disorder; osteoarthritis; cartilage defect; human;
XX tissue repair; gene therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..22 "signal peptide"
XX Peptide 15..23
XX Peptide /note= "immunogenic epitope"
XX Protein 23..297
XX Peptide /note= "mature protein"
XX Peptide 34..39
XX Peptide /note= "immunogenic epitope"
XX Peptide 51..57
XX Peptide /note= "immunogenic epitope"
XX Peptide 60..66
XX Peptide /note= "immunogenic epitope"
XX Peptide 153..158
XX Peptide /note= "immunogenic epitope"
XX Peptide 234..240
XX Peptide /note= "immunogenic epitope"
XX Peptide 269..274
XX Peptide /note= "immunogenic epitope"
XX Peptide 281..290
XX Peptide /note= "immunogenic epitope"
XX
XX WO200004183-A1.
XX
XX 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-US15783.
XX
XX 15-JUL-1998; 98US-0092922.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Young PE;
XX
XX WPI; 2000-182442/16.
XX N-PSDB; AA248600.
XX
XX Novel cDNA encoding human bone morphogenic proteins, vectors, host
XX cells and methods of recombinant production, useful for diagnosis and
XX treatment of, e.g. bone disorders -
XX
XX Claim 11; Page 184-185; 187pp; English.
XX
XX The invention provides novel human bone morphogenic proteins (BMP) and
XX nucleic acids encoding the BMPs. The BMP polypeptides can be expressed
XX by standard recombinant methodology. Determining the presence or absence
XX of a mutation in the polynucleotides or determining the presence or
XX amount of expression of the polypeptides is useful for diagnosing a
XX pathological condition or a susceptibility to a pathological condition
XX in a subject. The polynucleotides can also be used to prevent, treat or
XX ameliorate a medical condition. The proteins are useful for diagnosis
XX and/or treatment of diseases associated with BMPs, in particular bone
XX disorders (e.g. osteoarthritis, cartilage defects and tissue repair),
XX and in particular for stimulation of angiogenesis. The polynucleotides
XX are useful as reagents for differential identification of tissues or cell
XX types present in biological samples. The polynucleotides can be used in

```

CC gene therapy to promote the growth of endothelial cells. The present
 CC sequence represents a BMP of the invention (clone HSYA36).
 XX
 SQ Sequence 297 AA:
 Query Match 57.5%; Score 42; DB 21; Length 297;
 Best Local Similarity 42.9%; Pred. No. 12;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 OY 2 DRIVSIRTRGOIHS 15
 :|:::| | | | |
 Db 67 ERITVSTNGSIHS 80
 RESULT 20
 AAU02751 standard; Protein: 305 AA.
 ID AAU02751
 AC AAU02751:
 XX
 XX 29-AUG-2001 (first entry)
 DT
 XX Novel Human Protein, NHP #3.
 DE
 XX Human: Novel Human Protein: NHP; diagnostic: drug screening; cancer;
 KW clinical trial monitoring; physiological disorder; behavioural disorder;
 KW infectious disease; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX MO200129084-A2.
 PN
 XX 26-APR-2001.
 PD
 XX 18-OCT-2000; 2000MO-US28803.
 PE
 XX 18-OCT-1999; 99US-0160106.
 PR 29-OCT-1999; 99US-0162547.
 BR
 XX (LEXI-) LEXICON GENETICS INC.
 PA
 XX Turner CA, Donoho G, Nehls M, Hilbun E, Zambrowicz B, Sands AT;
 FI
 XX WPI: 2001-290898/30.
 DR N-PSDB: AAS03539.
 DK
 XX Nucleic acids encoding novel human proteins (NHP), useful for treating
 PT physiological or behavioural disorders, cancers and infectious diseases
 PT
 XX
 PS Claim 6; Page 62; 63pp; English.
 CC The sequence represents the amino acid sequence of novel human protein,
 CC NHP #3, isolated from a human adrenal gland cDNA library. NHP nucleotides
 CC are useful for drug screening and clinical trial monitoring, and for the
 CC diagnosis and treatment of physiological or behavioural disorders, cancer
 CC and infectious disease. Nucleotide constructs encoding functional NHPs,
 CC mutant NHPs, as well as antisense and ribozyme molecules can also be used
 CC in gene therapy for the modulation of NHP expression. NHP polypeptides
 CC may be used to produce agonists, antagonists and antibodies for the
 CC regulation of NHP expression in the treatment and/or diagnosis of
 CC disease.
 CC
 XX
 XX Sequence 305 AA:
 Query Match 57.5%; Score 42; DB 22; Length 305;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 OY 2 DRIVSIRTRGOIHS 15
 :|:::| | | | |
 Db 47 ERITVSTNGSIHS 60

RESULT 21
 AA84558
 ID AA84558 standard; Protein: 318 AA.
 AC
 XX AA84558:
 XX
 XX 25-JUL-2000 (first entry)
 DT
 XX A fragment of platelet-derived growth factor C (PDGF-C).
 DE
 XX Platelet-derived growth factor C; PDGF-C; cell proliferation;
 KW growth factor; heparin; connective tissue; wound healing; VEGF-F;
 KW fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth;
 KW choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia;
 KW lung carcinoma; erythroleukemia; tissue remodelling.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 287
 FT
 FT
 XX
 XX MO20018212-A2.
 PN
 XX 06-APR-2000.
 PD
 XX 30-SEP-1999; 99MO-US22668.
 PE
 XX 30-SEP-1998; 98US-0102461.
 PR 12-NOV-1998; 98US-0108109.
 PR 03-DEC-1998; 98US-0110749.
 PR 18-DEC-1998; 98US-0113002.
 PR 21-MAY-1999; 98US-0135426.
 PR 15-JUL-1999; 99US-0144022.
 XX
 XX (LUDM-) LUDMIG INST CANCER RES.
 PA (UTHE-) UNIV HELSINKI LICENSING LTD.
 XX
 XX Eriksson U, Aase K, Lee X, Ponten A, Uutela M, Alltalo K;
 FI
 XX Betschman A, Heidn C, Betscholz C;
 DT
 XX WPI: 2000-292954/25.
 DR N-PSDB: AAA12524.
 DK
 XX Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation,
 PT differentiation, growth and motility of cells expressing the PDGF-C
 PT receptor -
 PT
 XX
 XX Disclosure; Fig 4; 135pp; English.
 CC The present sequence represents a human platelet-derived growth factor C
 CC (PDGF-C) (formally designated VEGF-F) fragment. PDGF-C polypeptides have
 CC the ability to stimulate and enhance proliferation or differentiation,
 CC and/or growth or motility of cells expressing a PDGF-C receptor.
 CC PDGF-C polypeptides can be used in pharmaceuticals for promoting cell
 CC proliferation, preferably in combination with one other growth factor
 CC and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also
 CC be used for stimulating connective tissue or wound healing. The
 CC PDGF-C polypeptide can be enzymatically processed to generate the active
 CC truncated form of PDGF-C. PDGF-C can also be used to regulate the receptor-binding
 CC specificity of PDGF-C. PDGF-C can also be used to promote fibroblast
 CC mitogenesis in a mammal and to induce PDGF alpha receptor activation.
 CC PDGF-C antagonists can be used to inhibit tumour growth of a tumour
 CC expressing PDGF-C in a mammal. Specific types of human tumours, e.g.
 CC choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
 CC and erythroleukemia, can be identified by testing for expression of
 CC PDGF-C. PDGF-C antagonists can also be used to inhibit tissue
 CC remodelling during invasion of tumour cells into a normal population of
 CC cells. Antagonists can also be used to treat fibrotic conditions,
 CC especially found in the lung, kidney or liver.
 CC
 XX
 XX Sequence 318 AA:
 SQ

Query Match 57.5%; Score 42; DB 21; Length 318;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DRVLSIRTRGQIHS 15
 :|:::| | | | |
 Db 20 ERITVSTNGSIHS 33

RESULT 22

AAB58438
 ID AAB58438 standard; Protein; 339 AA.

AC AAB58438;

DT 14-MAR-2001 (first entry)

DE Lung cancer associated polypeptide sequence SEQ ID 776.

XX Human; lung cancer associated protein; neuroprotective; cytostatic;

KW cardiactive; immunomodulatory; muscular active; vulnery;

KW gastrointestinal; nephrotropic; antiinfective; gynecological;

KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;

KW proliferative disorder; wound healing; infectious disease.

OS Homo sapiens.

PN WO20005180-A2.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US05918.

PR 12-MAR-1999; 99US-0124270.

PI (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

PI Ruben SM;

XX WPI: 2000-587514/55.

DR N-PSDB; AAF18314.

XX Claim 11; Page 1305-1306; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer

XX associated proteins represented in AAB58106 - AAB58548. Lung cancer

XX associated proteins and polynucleotide sequences, their agonists, and

XX antagonists may have neuroprotective; cytostatic; cardiactive;

XX immunomodulatory; muscular active general; vulnery; gastrointestinal

XX general; nephrotropic; antiinfective; gynecological; or antibacterial

XX activity. The invention also includes antibodies specific for the

XX protein or polynucleotide sequences. The lung cancer associated

XX polynucleotide sequences may be used for detection of lung cancer,

XX chromosome identification, as chromosome markers, and for numerous other

XX diagnostic or research purposes. The proteins may be used to treat

XX disorders such as neural, immune, muscular, reproductive,

XX gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

XX disorders. The proteins may also be used in the treatment of wounds and

XX infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and

XX peptide AAB5549 are used in the course of the invention for the

XX identification and characterisation of the polynucleotide and protein

XX sequences.

XX Sequence 339 AA;

XX Query Match 57.5%; Score 42; DB 21; Length 339;

XX Best Local Similarity 42.9%; Pred. No. 14;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DRVLSIRTRGQIHS 15
 :|:::| | | | |
 Db 41 ERITVSTNGSIHS 54

RESULT 23

AAV33679

ID AAV33679 standard; Protein; 345 AA.

XX AAV33679;

DT 11-JAN-2000 (first entry)

DE Human VEGF-E protein.

XX VEGF-E; human; vascular endothelial cell growth factor; wound repair;

KW treatment; cardiovascular disorder; endothelial disorder; therapy;

KW tissue generation; regeneration; cardiac hypertrophy; cancer; detection;

KW angiogenic disorder; age-related macular degeneration; vascular disease;

XX neovascularization; tumor; gene mapping.

OS Homo sapiens.

PN WO947677-A2.

PD 23-SEP-1999.

PF 10-MAR-1999; 99WO-US05190.

PR 17-MAR-1998; 98US-0040220.

PR 02-NOV-1998; 98US-0184216.

PA (GETH) GENENTECH INC.

PI Ferrara N, Kuo SS;

XX WPI: 1999-560306/49.

DR N-PSDB; AA223691.

XX New growth factor polypeptide useful for treating cardiovascular or

XX endothelial disorders, e.g. cardiac hypertrophy -

XX Claim 1; Fig 2; 122pp; English.

XX This invention describes the isolation of a novel human vascular

XX endothelial cell growth factor-E (VEGF-E) polypeptide which has

XX tranquilizer, vulnery and cardiant activity. VEGF-E can be administered

XX therapeutically, especially by expressing encoding polynucleotides, to

XX treat cardiovascular or endothelial disorders in mammals, especially

XX humans. It is useful in wound repair and tissue generation and

XX regeneration, and may especially be used to treat cardiac hypertrophy

XX It can be combined with a carrier in pharmaceutical compositions, which

XX can be administered to treat disorders as above. VEGF-E can be used to

XX screen for antagonists and agonists, and the antagonists administered to

XX treat angiogenic disorders in mammals (especially humans) e.g. cancer or

XX age-related macular degeneration. It can be used to generate antibodies,

XX useful to detect VEGF-E polypeptide, as above. The antibodies are also

XX useful to detect VEGF-E polypeptide, especially to diagnose

XX cardiovascular, endothelial or angiogenic disorders in mammals (e.g.

XX vascular disease, or neovascularization associated with tumor formation),

XX by contacting the antibody with a tissue sample and detecting formation

XX of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding

XX VEGF-E can be used to diagnose cardiovascular and endothelial disorders

XX in mammals, by detecting abnormally high or low VEGF-E gene expression in

XX tissue samples. They can also be used to diagnose a disease or

XX susceptibility to a disease related to a mutated form of VEGF-E (e.g. a

XX cardiovascular, endothelial or angiogenic disorder such as a tumor), by

XX detecting a mutation in the VEGF-E-encoding sequence isolated from a

XX sample. They may also be used to produce probes useful to detect related

XX sequences or for gene mapping. This sequence represents the human VEGF-E

XX protein described in the method of the invention.

CC invention.
 XX
 SQ Sequence 345 AA;
 Query Match 57.5%; Score 42; DB 20; Length 345;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRQIHS 15
 :|:::| | | | |
 Db 47 ERITVSTNGSIHS 60

RESULT 25
 AAY30023
 ID AAY30023 standard; Protein: 345 AA.
 XX
 AC AAY30023;
 XX
 DT 11-OCT-1999 (first entry)
 XX
 DE Human vascular endothelial growth factor related protein.
 XX
 KW Vascular endothelial growth factor related protein; VEGF-R protein;
 KW tissue growth inhibition; tumour growth; cancer; tissue growth;
 KW angiogenesis; coronary artery blockage.
 XX
 OS Homo sapiens.
 XX
 PN MO9937671-A1.
 XX
 PD 29-JUL-1999.
 XX
 PE 26-JAN-1999; 99WO-US01574.
 XX
 PR 31-AUG-1998; 98US-0098548.
 PR 27-JAN-1998; 98US-0072635.
 PR 05-JUN-1998; 98US-0088089.
 PR 24-JUN-1998; 98US-0090544.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Dou S, Na S, Song HY;
 XX
 DR WPI: 1999-458680/38.
 DR N-PSDB; AAX86352.
 XX
 PT A vascular endothelial growth factor related protein and related
 PT polynucleotide, useful for identifying antagonists and binding
 PT compounds
 PT
 PS Claim 1; Page 56-58; 62pp; English.
 XX
 CC The present sequence represents a vascular endothelial growth factor
 CC related (VEGF-R) protein. VEGF-R can be used in assays to identify
 CC compounds that bind to it or that antagonize its activity. VEGF-R
 CC antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting
 CC tissue growth. This is useful for inhibiting tumour growth and for
 CC treating cancer. VEGF-R itself can be used to stimulate tissue
 CC growth, angiogenesis and to treat coronary artery blockage. The
 CC VEGF-R coding sequence can be used for the recombinant production of
 CC the VEGF-R protein.
 CC
 XX
 SQ Sequence 345 AA;
 Query Match 57.5%; Score 42; DB 20; Length 345;
 Best Local Similarity 42.9%; Pred. No. 15;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRQIHS 15
 :|:::| | | | |
 Db 47 ERITVSTNGSIHS 60

RESULT 26
 AAB48657
 ID AAB48657 standard; Protein: 345 AA.
 XX
 AC AAB48657;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human zvegfg3, SEQ ID NO:33.
 XX
 DE Human zvegfg3, SEQ ID NO:33.
 XX
 KW Human: zvegfg3; zvegfg4 fusion; growth factor homologue; VEGF/PDGF family;
 KW CUB domain; PDGF-like activity; mitogenic; osteogenic;
 KW neovascularisation; tissue repair; proliferation; differentiation;
 KW liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
 KW periodontal disease; bone fracture; wound healing; vulnerability; ischaemia;
 KW immunomodulation; hepatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200066736-A1.
 XX
 PD 09-NOV-2000.
 XX
 PE 03-MAY-2000; 2000WO-US40047.
 XX
 PR 03-MAY-1999; 99US-0304216.
 PR 10-NOV-1999; 99US-0164463.
 PR 04-FEB-2000; 2000US-0180169.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
 XX
 DR WPI: 2000-687541/67.
 DR N-PSDB; AAC81582.
 XX
 PT Growth factor homologs and the nucleic acids that encode them, useful
 PT e.g. for treating liver damage, ischaemia, multiple sclerosis and
 PT Alzheimer's disease -
 PT
 PS Claim 48; Page 125-126; 143pp; English.
 XX
 CC The invention relates to the human growth factor homologue zvegfg4
 CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegfg4 is a member
 CC of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial
 CC growth factor) family. Zvegfg4 has a growth factor domain (AAB48654)
 CC characterised by a PDGF cystine knot structure, and a CUB domain
 CC (AAB48655) which has a beta barrel structure. Zvegfg4 has PDGF-like
 CC activity, having mitogenic activity on fibroblasts, vascular smooth
 CC muscle cells and pericytes, and has also been shown to stimulate bone
 CC growth. The invention also relates to fusion proteins comprising human
 CC zvegfg4 or fragments thereof, particularly human zvegfg4/human zvegfg3
 CC fusions; expression constructs and host cells comprising human zvegfg4
 CC nucleic acids; the recombinant expression of human zvegfg4; an antibody
 CC which binds to human zvegfg4 or a fragment thereof; a method of activating
 CC a cell-survive PDGF receptor using a zvegfg4-derived polypeptide; a
 CC method of modulating the proliferation, differentiation, migration or
 CC metabolism of bone cells, comprising exposing bone cells to
 CC zvegfg4-derived polypeptides; and a method of detecting a genetic
 CC abnormality in the zvegfg4 gene of a patient. Zvegfg4 proteins and derived
 CC fragments may be used to stimulate tissue development or repair, or
 CC cellular differentiation or proliferation. They are particularly used for
 CC the treatment or repair of liver damage, and may also be used to
 CC modulate neurite growth (e.g., in the treatment of Alzheimer's disease or
 CC multiple sclerosis). Due to their osteogenic activity, they may also be
 CC used in the treatment of periodontal disease and fractures. They may also be
 CC used to enhance expansion and mobilisation of haematopoietic stem cells
 CC and endothelial precursor stem cells, which may be useful in the
 CC treatment of ischaemia, in wound healing, and in the modulation of the
 CC immune system. The present sequence represents human zvegfg3.
 CC
 XX
 SQ Sequence 345 AA;

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVIRTRGOIHS 15
:||||:| | | | |
DB 47 ERITVSTNGSIHS 60

RESULT 27
AAB24250
ID AAB24250 standard; Protein; 345 AA.
XX
AC AAB24250;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human platelet-derived growth factor related protein LP8.
XX
DE Human: platelet derived growth factor related protein; LP8; VEGFh.
KW vascular endothelial growth factor h; tissue regeneration; vulnerrary;
XX atherosclerosis; PDGF-related protein; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PM W0200059940-R2.
XX
PD 12-OCT-2000.
XX
PF 24-MAR-2000; 2000MO-US06427.
XX
PR 06-APR-1999; 9905-0127913.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Hammond LJ, Na S;
XX
DR WPI: 2000-664991/64.
XX
N-PSDB: AAC64426.
XX
PT Enhancing tissue growth and promoting wound healing by administering
XX platelet-derived growth factor related protein, LP8 or its analog
XX treating atherosclerosis by administering LP8 antagonist
XX
PS Claim 4; Page 63-64; 64pp; English.
XX
CC The present invention describes a method for enhancing tissue growth,
XX promoting wound healing or stimulating smooth muscle growth by
XX administering a platelet-derived growth factor (PDGF) related protein,
XX designated LP8 or its analogue. Also described is a method of slowing
XX the progress of atherosclerosis or treating atherosclerosis comprising
XX the administration of an LP8 antagonist. The method is useful for
XX enhancing tissue growth, promoting wound healing and stimulating smooth
XX muscle growth. Antagonists of LP8 are useful for treating
XX atherosclerosis. The present sequence represents human LP8, which is
XX also called VEGFh.
XX
SQ Sequence 345 AA;
XX

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVIRTRGOIHS 15
:||||:| | | | |
DB 47 ERITVSTNGSIHS 60

RESULT 28
AAB44322
ID AAB44322 standard; Protein; 345 AA.

AC AAB44322;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
XX
XX
KW Human: secreted protein; transmembrane protein; PRO; EGF; cytosstatic;
XX expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN W0200053756-R2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000MO-US04341.
XX
PR 08-MAR-1999; 99MO-US05028.
XX
PR 12-MAR-1999; 99US-0123957.
XX
PR 29-MAR-1999; 99US-0126773.
XX
PR 21-APR-1999; 99US-0130232.
XX
PR 28-APR-1999; 99US-0131445.
XX
PR 14-MAY-1999; 99US-0134287.
XX
PR 23-JUN-1999; 99US-0141037.
XX
PR 26-JUL-1999; 99US-0145898.
XX
PR 28-OCT-1999; 99US-0162506.
XX
PR 30-NOV-1999; 99MO-US28313.
XX
PR 02-DEC-1999; 99MO-US28351.
XX
PR 02-DEC-1999; 99MO-US28365.
XX
PR 16-DEC-1999; 99MO-US30095.
XX
PR 30-DEC-1999; 99MO-US31243.
XX
PR 30-DEC-1999; 99MO-US31274.
XX
PR 05-JAN-2000; 2000MO-US00219.
XX
PR 06-JAN-2000; 2000MO-US00277.
XX
PR 06-JAN-2000; 2000MO-US00376.
XX
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers LJ, Eaton DL;
XX
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX
PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
XX
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
XX
DR WPI: 2000-611443/58.
XX
DR N-PSDB: AAC78582.
XX
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities -
XX
PS Claim 12; Fig 207; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 345 AA;
XX

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVIRTRGOIHS 15
:||||:| | | | |

Db 47 ERITVSTNGSIHS 60

RESULT 29
AAB10633
ID AAB10633 standard; Protein: 345 AA.
XX
AC AAB10633;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytosstatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR N-PSDB: AAA71951.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 6; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytosstatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the RACE generated human VEGF-X
CC protein described in the method of the invention.
XX
SQ Sequence 345 AA;

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSIIRTRQGIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

RESULT 30
AAB10634
ID AAB10634 standard; Protein: 345 AA.
XX
AC AAB10634;
XX
DT 19-JAN-2001 (first entry)
XX
DE Human VEGF-X homologue protein.
XX
KW VEGF-X; vascular endothelial growth factor; human; vulnary; cytosstatic;
KW antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment;
KW angiogenesis regulator; vascularization regulator; cancer; psoriasis;
KW rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair;
KW tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore;
KW venous sore; diabetic ulcer; burns; skin graft growth.
XX
OS Homo sapiens.
XX
PN WO200037641-A2.
XX
PD 29-JUN-2000.
XX
PF 21-DEC-1999; 99WO-US30503.
XX
PR 22-DEC-1998; 98GB-0028377.
PR 18-MAR-1999; 99US-0124967.
PR 08-NOV-1999; 99US-0164131.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Gordon RD, Sprengel JJ, Yon JR, Dijkmans JJH, Gosiowska A;
PI Dhanaraj SN, Xu J;
XX
DR WPI: 2000-442669/38.
DR N-PSDB: AAA71952.
XX
PT New vascular endothelial growth factor protein, useful for treating or
PT preventing diseases associated with inappropriate angiogenesis activity
PT such as cancer, rheumatoid arthritis, psoriasis and wounds -
XX
PS Disclosure; Fig 7; 127pp; English.
XX
CC This invention describes a novel vascular endothelial growth factor-X
CC (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has
CC vulnary, cytosstatic, antirheumatic, antiarthritic, antipsoriatic and
CC antidiabetic activity and acts as an angiogenesis and vascularization
CC regulator. An antisense molecule of the invention is useful for treating
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic
CC retinopathy by inhibiting angiogenic activity or inappropriate
CC vascularization including formation and proliferation of new blood
CC vessels, growth and development of tissues, tissue regeneration and organ
CC and tissue repair in a subject. The products of the invention are useful
CC for preparing medicaments for treating wounds such as dermal ulcers,
CC pressure sores, venous sores, diabetic ulcers and burns and to promote
CC skin graft growth, tissue repair, proliferation of new blood vessels,
CC tissue regeneration and organ repair by promoting angiogenic activity or
CC vascularization. This sequence represents the human VEGF-X protein
CC homologue described in the method of the invention.
XX
SQ Sequence 345 AA;

Query Match 57.5%; Score 42; DB 21; Length 345;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRVSIIRTRQGIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

Search completed: August 29, 2003, 18:43:56

Wed Sep 3 13:06:20 2003

us-09-830-876-1_1.rag

Page 17

Job time : 48.8571 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:38:06 ; Search time 15.8571 Seconds
(without alignments)
40.024 Million cell updates/sec

Title: US-09-830-876-1
Perfect score: 73
Sequence: 1 IDRLVSRTRQIHS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
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| 2 | 45 | 61.6 | 428 | 1 | US-08-343-380-4 |
| 3 | 45 | 61.6 | 428 | 3 | US-09-072-435-4 |
| 4 | 45 | 61.6 | 428 | 3 | US-09-072-917A-4 |
| 5 | 45 | 61.6 | 434 | 1 | US-07-923-692C-6 |
| 6 | 45 | 61.6 | 434 | 1 | US-08-184-227C-6 |
| 7 | 45 | 61.6 | 434 | 2 | US-08-482-220-6 |
| 8 | 45 | 61.6 | 434 | 3 | US-08-484-341-6 |
| 9 | 45 | 61.6 | 434 | 3 | US-08-483-502-6 |
| 10 | 45 | 61.6 | 434 | 3 | US-09-726-651A-6 |
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| 14 | 45 | 57.5 | 345 | 4 | US-09-040-220D-2 |
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| 17 | 45 | 57.5 | 345 | 4 | US-09-540-224-5 |
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| 28 | 39 | 53.4 | 446 | 3 | US-09-909-325-2 |
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| 35 | 39 | 53.4 | 461 | 5 | PCT-US95-13924-2 |
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| 98 | 33 | 45.2 | 168 | 4 | US-09-198-452A-1079 |
| 99 | 33 | 45.2 | 239 | 4 | US-09-252-991A-21942 |
| 100 | 33 | 45.2 | 239 | 4 | US-09-252-991A-21942 |

ALIGNMENTS

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RESULT 1
US-07-973-324A-4
; Sequence 4, Application US/07973324A
; Patent No. 5460952
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,324A
; FILING DATE: 04-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-973-324A-4
Query Match 61.6%; Score 45; DB 1; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIH 14
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Db 359 IERLVSIRNRQGIH 372

RESULT 2
US-08-343-380-4
; Sequence 4, Application US/08343380
; Patent No. 5712112
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,380
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-343-380-4
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Query Match 61.6%; Score 45; DB 1; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 IDRLVSIRTRGQIH 14
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Db 359 IERLVSIRNRQGIH 372

RESULT 3
US-09-072-435-4
; Sequence 4, Application US/09072435
; Patent No. 6215051
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
; TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072,435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/639,792
; FILING DATE: 29-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
```

REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match 61.6%; Score 45; DB 3; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRRGQIH 14
DB 359 IERLVSTRNRGQIH 372

RESULT 4
US-09-072-917A-4

Sequence 4, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Iu, Su-May
APPLICANT: Iu, Lu-Tse
APPLICANT: Chau, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gersteln, Murray & Borun
STREET: 235 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match 61.6%; Score 45; DB 3; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.78;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRRGQIH 14
DB 359 IERLVSTRNRGQIH 372

RESULT 5
US-07-923-692C-6

Sequence 6, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Tulpen, Thomas H.
APPLICANT: Tulpen, Ann Myers
APPLICANT: Gager, Stephen J.
APPLICANT: Gail, Lawrence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
TITLE OF INVENTION: 11
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-8716
TELEFAX: 415-433-4150
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-6

Query Match 61.6%; Score 45; DB 1; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRRGQIH 14
I:|||||I|I|
Db 365 IERLVSTRRGQIH 378

RESULT 6

US-08-184-237-6
; Sequence 6, Application US/08184237
; Patent No. 5589367
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lambach & Lambach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CAL
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,237
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 923,692
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: BIOG-20121 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-184-237-6

Query Match 61.6%; Score 45; DB 1; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSTRRGQIH 14
I:|||||I|I|
Db 365 IERLVSTRRGQIH 378

RESULT 7

US-08-482-920-6
; Sequence 6, Application US/08482920
; Patent No. 5866785
; GENERAL INFORMATION:
; APPLICANT: Donson, Jon
; APPLICANT: Dawson, William O.
; APPLICANT: Grantham, George L.
; APPLICANT: Turpen, Thomas H.
; APPLICANT: Turpen, Ann Myers
; APPLICANT: Garger, Stephen J.
; APPLICANT: Grill, Laurence K.
; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,920
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 184,237
; FILING DATE: 19-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,244
; FILING DATE: 22-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 641,617
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 310,881
; FILING DATE: 17-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,766
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 160,771
; FILING DATE: 26-FEB-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 347,637
; FILING DATE: 05-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 363,138
; FILING DATE: 08-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 219,279
; FILING DATE: 15-JUL-1988
; ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-6

Query Match 61.6%; Score 45; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRNGQIH 14
|:|||||:|
Db 365 IERLVSIIRNGQIH 378

RESULT 8
US-08-484-341-6
Sequence 6, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lambach & Lambach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <Unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-484-341-6

Query Match 61.6%; Score 45; DB 3; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRNGQIH 14
|:|||||:|
Db 365 IERLVSIIRNGQIH 378

RESULT 9
US-08-483-502-6
Sequence 6, Application US/08483502
Patent No. 6284492
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
Dawson, William O.
Grantham, George L.
Turpen, Thomas H.
Turpen, Ann Myers
Garger, Stephen J.
Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,502
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/739,143
FILING DATE:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957

APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219, 279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-6

Query Match 61.6%; Score 45; DB 3; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
:||||| |
Db 365 IERLVSIRTRGOIH 378

RESULT 10
US-09-726-651A-6
Sequence 6, Application US/09726651A
Patent No. 6448046
GENERAL INFORMATION:
APPLICANT: Dawson, William O.
APPLICANT: GRANTHAM, GEORGE L.
APPLICANT: TURPEN, Thomas H.
APPLICANT: TURPEN, Ann M.
APPLICANT: GARGER, Stephen J.
APPLICANT: GRILL, Laurence K.
TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
FILE REFERENCE: 008010023CNU01
CURRENT APPLICATION NUMBER: US/09/726, 651A
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 08/483,502
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/184,237
PRIOR FILING DATE: 1994-01-19
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 434
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: CLONE: alpha-amylase
OTHER INFORMATION: protein
US-09-726-651A-6

Query Match 61.6%; Score 45; DB 4; Length 434;
Best Local Similarity 71.4%; Pred. No. 0.79;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14

Db 365 IERLVSIRTRGOIH 378

RESULT 11
US-09-198-452A-959
Sequence 959, Application US/09198452A
Patent No. 6559284
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 959
LENGTH: 460
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: SITE
LOCATION: 1...460
OTHER INFORMATION: Xaa-unknown or other
US-09-198-452A-959

Query Match 60.3%; Score 44; DB 4; Length 460;
Best Local Similarity 57.1%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
|||:| | |
Db 407 DRLVSIRTRGOIHS 420

RESULT 12
US-09-564-595D-54
Sequence 54, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOGY ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion polypeptide
US-09-564-595D-54

Query Match 57.5%; Score 42; DB 4; Length 302;
Best Local Similarity 42.9%; Pred. No. 2.1;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
:|:|:| | | |
Db 2 ERLTWTGSIHS 15


```
RESULT 13
US-09-564-595D-55
; Sequence 55, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Shepherd, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-09-564-595D-55

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 316;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGOIHS 15
DB 2 ERITVSTNGSIHS 15

RESULT 14
US-09-040-220D-2
; Sequence 2, Application US/09040220D
; Patent No. 6391311
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
; FILE REFERENCE: P1122
; CURRENT APPLICATION NUMBER: US/09/040,220D
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-040-220D-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGOIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 15
US-09-457-066-2
; Sequence 2, Application US/09457066
; Patent No. 6432673
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
US-09-457-066-2

APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Shepherd, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/09/457,066
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-457-066-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGOIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 16
US-09-265-686-2
; Sequence 2, Application US/09265686
; Patent No. 6455283
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
; FILE REFERENCE: P1122P2
; CURRENT APPLICATION NUMBER: US/09/265,686
; CURRENT FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: US 09/040,220
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: US 09/184,216
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Human
US-09-265-686-2

Query Match
Best Local Similarity 57.5%; Score 42; DB 4; Length 345;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGOIHS 15
DB 47 ERITVSTNGSIHS 60

RESULT 17
US-09-540-224-5
; Sequence 5, Application US/09540224
; Patent No. 6468543
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Hart, Charles E.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
; FILE REFERENCE: 00-28
; CURRENT APPLICATION NUMBER: US/09/540,224
; CURRENT FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: US 60/180,169
; EARLIER FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 9
US-09-540-224-5
```

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-540-224-5

```

```

Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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```

QY      2 DLVSIIRTRQIHS 15
       :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

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RESULT 18
US-09-564-595D-33
; Sequence 33, Application US/09564595D
; Patent No. 6495668
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/564,595D
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-595D-33

```

```

Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 DLVSIIRTRQIHS 15
       :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

```

RESULT 19
US-09-706-968-2
; Sequence 2, Application US/09706968
; Patent No. 6528050
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
; CURRENT FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: US/09/541,752
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-706-968-2

```

```

Query Match          57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 2.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 DLVSIIRTRQIHS 15
       :|:::| | | |
Db      47 ERITVSTNGSIHS 60

```

```

RESULT 20
US-08-466-120-2
; Sequence 2, Application US/08466120
; Patent No. 5869284
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoid Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,120
; FILING DATE: June 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07266
; FILING DATE: 24 JUN 94
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 433 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-466-120-2

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Query Match          53.4%; Score 39; DB 2; Length 433;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY      3 RLVSIRTRQIHS 15
       :|:::| | | |
Db      396 KLVSLRTSSVHS 408

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RESULT 21
PCT-US94-07266-2
; Sequence 2, Application PC/TUS9407266
; GENERAL INFORMATION:
; APPLICANT: CAO, ET AL.
; TITLE OF INVENTION: Retinoid Acid Receptor Epsilon
; NUMBER OF SEQUENCES: 2

```

CORRESPONDENCE ADDRESS:
ADDRESSER: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07266
FILING DATE: Concurrently
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 AMINO ACIDS
TYPE: AMINO ACID
STRANDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-07266-2

Query Match 53.4%; Score 39; DB 5; Length 433;
Best local similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIRFGQIHS 15
DB 396 KLVSLRTLSVHS 408

RESULT 22
US-08-333-358-8
Sequence 8, Application US/08333358
Patent No. 5571696
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,358

FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-358-8

Query Match 53.4%; Score 39; DB 1; Length 440;
Best local similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIRFGQIHS 15
DB 403 KLVSLRTLSVHS 415

RESULT 23
US-08-463-694-8
Sequence 8, Application US/08463694
Patent No. 5666233
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,694
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-694-8

Query Match 53.4%; Score 39; DB 1; Length 440;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
DB 403 KLVSLRTLSSVHS 415

RESULT 24
US-08-694-501-8
Sequence 8, Application US/08694501
Patent No. 5710004
GENERAL INFORMATION:

APPLICANT: EVANS, Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG MS., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO Mr., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA

COUNTRY: US
ZIP: 90071-2921

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/694,501

FILING DATE: 07-AUG-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/333,358

FILING DATE:

APPLICATION NUMBER: US/07/761,068

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Reiter Ph.D., Stephen E.

REGISTRATION NUMBER: 31192

REFERENCE/DOCKET NUMBER: P31 8936

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 440 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-694-501-8

Query Match 53.4%; Score 39; DB 1; Length 440;

Best Local Similarity 53.8%; Pred. No. 12;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
DB 403 KLVSLRTLSSVHS 415

RESULT 25

US-08-342-411A-4
Sequence 4, Application US/08342411A
Patent No. 5639616
GENERAL INFORMATION:

APPLICANT: LIAO, Shutsung
APPLICANT: SONG, Ching
TITLE OF INVENTION: UBIDOUTOUS NUCLEAR RECEPTOR:
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,411A

FILING DATE: 18-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KITCHELL, BARBARA S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: ARCD154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

INFORMATION FOR SEQ. ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-342-411A-4

Query Match 53.4%; Score 39; DB 1; Length 443;

Best Local Similarity 53.8%; Pred. No. 13;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRQIHS 15
:||||:||||
DB 406 KLVSLRTLSSVHS 418

RESULT 26
US-08-372-652-3

Sequence 3, Application US/08372652

Patent No. 5932699

GENERAL INFORMATION:

APPLICANT: Moore, David

APPLICANT: Choi, Hwang-sik

TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING

TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-652-3

Query Match 53.4%; Score 39; DB 2; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIPTRGQHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 27
US-08-776-844-2
Sequence 2, Application US/08776844
Patent No. 6277976
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,844
FILING DATE: 24-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03247
FILING DATE: 16-AUG-1995
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-776-844-2

Query Match 53.4%; Score 39; DB 3; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIPTRGQHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 28
US-09-909-325-2
Sequence 2, Application US/09909325
Patent No. 6525188
GENERAL INFORMATION:
APPLICANT: ENMARK, EVA
GUSTAFSSON, JAN
TITLE OF INVENTION: OR-1 ON ORPHAN RECEPTOR BELONGING
TO THE NUCLEAR RECEPTOR FAMILY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/909,325
FILING DATE: 19-JUL-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,844
FILING DATE: <unknown>
APPLICATION NUMBER: UK 9413536.2
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 00487.04029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-909-325-2

Query Match 53.4%; Score 39; DB 4; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIPTRGQHS 15
:|||||:|
DB 409 KLVSLRTLSVHS 421

RESULT 29
PCT-US95-16311-3
Sequence 3, Application PC/TUS9516311

GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Seol, Wongi
APPLICANT: Choi, Hwang-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16311-3

Query Match 53.4%; Score 39; DB 5; Length 446;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQIHS 15
DB 409 KLVSLRLTSSVHS 421

RESULT 30
US-08-373-935-1
Sequence 1, Application US/08373935
Patent No. 5747661
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Mangelsdorf, David J.
APPLICANT: Willy, Patricia J.
TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Prietly, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,935
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-4737
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-935-1

Query Match 53.4%; Score 39; DB 1; Length 447;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQIHS 15
DB 410 KLVSLRLTSSVHS 422

Search completed: August 29, 2003, 18:44:39
Job time : 17.8571 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:42:11 ; Search time 23.5714 Seconds

(without alignments)
87.043 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

Sequence: 1 IDRLVSIKRGQIHS 15

Scoring table: BLOSUM62

Gap: 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 45 | 61.6 | 434 | 12 | US-10-280-679B-6 |
| 2 | 42 | 57.5 | 117 | 10 | US-09-852-209A-19 |
| 3 | 42 | 57.5 | 117 | 15 | US-10-131-600-19 |
| 4 | 42 | 57.5 | 297 | 15 | US-10-103-197-5 |
| 5 | 42 | 57.5 | 318 | 10 | US-09-852-209A-5 |
| 6 | 42 | 57.5 | 318 | 15 | US-10-131-600-5 |
| 7 | 42 | 57.5 | 339 | 9 | US-09-925-302-776 |
| 8 | 42 | 57.5 | 345 | 9 | US-09-823-033-2 |
| 9 | 42 | 57.5 | 345 | 9 | US-09-818-943-1 |
| 10 | 42 | 57.5 | 345 | 9 | US-09-923-995-4 |
| 11 | 42 | 57.5 | 345 | 10 | US-09-795-006A-149 |
| 12 | 42 | 57.5 | 345 | 10 | US-09-978-295A-488 |
| 13 | 42 | 57.5 | 345 | 10 | US-09-852-209A-3 |
| 14 | 42 | 57.5 | 345 | 10 | US-09-978-697-488 |
| 15 | 42 | 57.5 | 345 | 10 | US-09-978-192A-488 |

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|----|----|------|-----|----|--------------------|-------------------|
| 16 | 42 | 57.5 | 345 | 10 | US-09-999-832A-488 | Sequence 488, App |
| 17 | 42 | 57.5 | 345 | 11 | US-09-978-189-488 | Sequence 488, App |
| 18 | 42 | 57.5 | 345 | 11 | US-09-796-753-6 | Sequence 6, App11 |
| 19 | 42 | 57.5 | 345 | 11 | US-09-978-608A-488 | Sequence 488, App |
| 20 | 42 | 57.5 | 345 | 11 | US-09-978-585A-488 | Sequence 488, App |
| 21 | 42 | 57.5 | 345 | 11 | US-09-978-191A-488 | Sequence 488, App |
| 22 | 42 | 57.5 | 345 | 11 | US-09-978-403A-488 | Sequence 488, App |
| 23 | 42 | 57.5 | 345 | 11 | US-09-978-564A-488 | Sequence 488, App |
| 24 | 42 | 57.5 | 345 | 11 | US-09-999-832A-488 | Sequence 488, App |
| 25 | 42 | 57.5 | 345 | 11 | US-09-981-912A-488 | Sequence 488, App |
| 26 | 42 | 57.5 | 345 | 11 | US-09-978-824-488 | Sequence 488, App |
| 27 | 42 | 57.5 | 345 | 11 | US-09-918-583A-488 | Sequence 488, App |
| 28 | 42 | 57.5 | 345 | 11 | US-09-978-423A-488 | Sequence 488, App |
| 29 | 42 | 57.5 | 345 | 11 | US-09-978-193A-488 | Sequence 488, App |
| 30 | 42 | 57.5 | 345 | 11 | US-09-999-830A-488 | Sequence 488, App |
| 31 | 42 | 57.5 | 345 | 11 | US-09-978-187B-488 | Sequence 488, App |
| 32 | 42 | 57.5 | 345 | 11 | US-09-978-757A-488 | Sequence 488, App |
| 33 | 42 | 57.5 | 345 | 11 | US-09-978-187B-488 | Sequence 488, App |
| 34 | 42 | 57.5 | 345 | 11 | US-09-978-757A-488 | Sequence 488, App |
| 35 | 42 | 57.5 | 345 | 12 | US-09-978-188A-488 | Sequence 488, App |
| 36 | 42 | 57.5 | 345 | 12 | US-09-978-298A-488 | Sequence 488, App |
| 37 | 42 | 57.5 | 345 | 12 | US-10-137-870-286 | Sequence 286, App |
| 38 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 39 | 42 | 57.5 | 345 | 12 | US-10-140-021-286 | Sequence 286, App |
| 40 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 41 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 42 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 43 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 44 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 45 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 46 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 47 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 48 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 49 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 50 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 51 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 52 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 53 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 54 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 55 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 56 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 57 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 58 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 59 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 60 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 61 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 62 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 63 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 64 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 65 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 66 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 67 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 68 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 69 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 70 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 71 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 72 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 73 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 74 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 75 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 76 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 77 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 78 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 79 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 80 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 81 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 82 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 83 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 84 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 85 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 86 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 87 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |
| 88 | 42 | 57.5 | 345 | 12 | US-10-140-018-286 | Sequence 286, App |

89 42 57.5 345 12 US-10-141-753-286 Sequence 286, App
90 42 57.5 345 12 US-10-141-758-286 Sequence 286, App
91 42 57.5 345 12 US-10-142-418-286 Sequence 286, App
92 42 57.5 345 12 US-10-142-420-286 Sequence 286, App
93 42 57.5 345 12 US-10-142-422-286 Sequence 286, App
94 42 57.5 345 12 US-10-142-427-286 Sequence 286, App
95 42 57.5 345 12 US-10-142-760-286 Sequence 286, App
96 42 57.5 345 12 US-10-143-030A-488 Sequence 488, App
97 42 57.5 345 12 US-10-145-821-286 Sequence 286, App
98 42 57.5 345 12 US-10-152-531-286 Sequence 286, App
99 42 57.5 345 12 US-10-127-840A-286 Sequence 286, App
100 42 57.5 345 12 US-10-142-424-286 Sequence 286, App

ALIGNMENTS

RESULT 1

US-10-280-679B-6

Sequence 6, Application US/10280679B

Publication No. US20030150019A1

GENERAL INFORMATION:

APPLICANT: Large Scale Biology Corporation

TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors

FILE REFERENCE: LSBC-0109-US03

CURRENT APPLICATION NUMBER: US/10/280,679B

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: 09/557,941

PRIOR FILING DATE: 2000-04-24

PRIOR APPLICATION NUMBER: 08/484,341

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 07/923,692

PRIOR FILING DATE: 1992-07-31

PRIOR APPLICATION NUMBER: 07/600,244

PRIOR FILING DATE: 1990-10-22

PRIOR APPLICATION NUMBER: 07/641,617

PRIOR FILING DATE: 1991-01-16

PRIOR APPLICATION NUMBER: 07/737,899

PRIOR FILING DATE: 1991-07-26

PRIOR APPLICATION NUMBER: 07/739,143

PRIOR FILING DATE: 1991-08-01

PRIOR APPLICATION NUMBER: 07/310,881

PRIOR FILING DATE: 1989-02-17

PRIOR APPLICATION NUMBER: 07/160,766

PRIOR FILING DATE: 1988-02-26

PRIOR APPLICATION NUMBER: 07/160,771

PRIOR FILING DATE: 1988-02-26

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 434

TYPE: PRT

ORGANISM: Rice alpha-amylase

US-10-280-679B-6

Query Match 61.6%; Score 45; DB 12; Length 434;
Best Local Similarity 71.4%; Pred. No. 4.1;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRRGQIH 14

DB 365 IERLVSIRRGQIH 378

RESULT 2

US-09-852-209A-19

Sequence 19, Application US/09852209A

Patent No. US20020164687A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LEE, Xuri

APPLICANT: PONTEN, Annica
APPLICANT: TUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-209A-19

Query Match 57.5%; Score 42; DB 10; Length 117;
Best Local Similarity 42.9%; Pred. No. 3.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IDRLVSIIRRGQIHS 15
DB 1 ERITVTGSGIHS 14

RESULT 3

US-10-131-600-19

Sequence 19, Application US/10131600

Publication No. US20030082670A1

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: AASE, Karin

APPLICANT: LEE, Xuri

APPLICANT: PONTEN, Annica

APPLICANT: TUTELA, Marko

APPLICANT: ALITALO, Kari

APPLICANT: OESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

APPLICANT: BETHSHOLTZ, Christer

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING

FILE REFERENCE: 09-410349-Eriksson et al-1064-44740

CURRENT APPLICATION NUMBER: US/10/131,600

PRIOR FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: US/09/410,349

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 60/108,109

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: 60/110,749

PRIOR FILING DATE: 1998-12-03

PRIOR APPLICATION NUMBER: 60/113,002

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: 60/135,426

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: 60/144,022

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 19

LENGTH: 117

TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-600-19

Query Match
Best Local Similarity 57.5%; Score 42; DB 15; Length 117;
Best Local Similarity 42.9%; Pred. No. 3.4;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRGOIHS 15
:|||||
Db 1 ERITVSTNGSIHS 14

RESULT 4

US-10-103-197-5
Sequence 5, Application US/10103197
Publication No. US20030032098A1

GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: Bone Morphogenic Proteins (BMP family)
FILE REFERENCE: PR012P1
CURRENT APPLICATION NUMBER: US/10/103,197
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/458,690
PRIOR FILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapiens
US-10-103-197-5

Query Match
Best Local Similarity 57.5%; Score 42; DB 15; Length 297;
Best Local Similarity 42.9%; Pred. No. 9.6;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRGOIHS 15
:|||||
Db 67 ERITVSTNGSIHS 80

RESULT 5

US-09-852-209A-5
Sequence 5, Application US/09852209A
Patent No. US20020164687A1

GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALLTALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
FILE REFERENCE: 09-410349-ERIKSSON et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-209A-5

Query Match
Best Local Similarity 57.5%; Score 42; DB 10; Length 318;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRGOIHS 15
:|||||
Db 20 ERITVSTNGSIHS 33

RESULT 6

US-10-131-600-5
Sequence 5, Application US/10131600
Publication No. US20030082670A1

GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: ALLTALO, Kari
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: BETHSHOLTZ, Christer
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-ERIKSSON et al-1064-44740
CURRENT APPLICATION NUMBER: US/10/131,600
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-600-5

Query Match
Best Local Similarity 57.5%; Score 42; DB 15; Length 318;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSTRGOIHS 15
:|||||
Db 20 ERITVSTNGSIHS 33

RESULT 7

US-09-925-302-776
Sequence 776, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104

```
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 776
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-776
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Query Match 57.5%; Score 42; DB 9; Length 339;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY 2 DRLVSIRTRGQIHS 15
:|:::| | | | |
DB 41 ERITVSTNGSIHS 54
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```
RESULT 8
US-09-823-033-2
; Sequence 2, Application US/09823033
; Patent No. US20020004225A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.
; APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
; FILE REFERENCE: 00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2
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Query Match 57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 DRLVSIRTRGQIHS 15
:|:::| | | | |
DB 47 ERITVSTNGSIHS 60
```

```
RESULT 9
US-09-818-943-1
; Sequence 1, Application US/09818943
; Patent No. US20020049987A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
; APPLICANT: LI, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: AASE, Karin
; APPLICANT: LI, Hong
; TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F
; FILE REFERENCE: 1064/48487
; CURRENT APPLICATION NUMBER: US/09/818,943
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,507
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 345
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-943-1
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Query Match 57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY 2 DRLVSIRTRGQIHS 15
:|:::| | | | |
DB 47 ERITVSTNGSIHS 60
```

```
RESULT 10
US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-995-4
```

```
Query Match 57.5%; Score 42; DB 9; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 DRLVSIRTRGQIHS 15
:|:::| | | | |
DB 47 ERITVSTNGSIHS 60
```

```
RESULT 11
US-09-795-006A-149
; Sequence 149, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Altalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 149
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-149
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```
Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY 2 DRLVSIRTRGQIHS 15
:|:::| | | | |
DB 47 ERITVSTNGSIHS 60
```

RESULT 12
US-09-978-295A-488
Sequence 488, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Macy E.
APPLICANT: Godowsky, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR APPLICATION NUMBER: 60/083496
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match      57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Db      47 ERLITVSTNGSIHS 60
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RESULT 13
US-09-852-209A-3
; Sequence 3, Application US/09852209A
; Patent No. US20020164687A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, ULF
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; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTEN, Annica
; APPLICANT: TUTTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: BETHSHOLTZ, Christer
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DNA CODING
; FILE REFERENCE: 09-410349-ERIKSSON ET AL-1064-44740
; CURRENT APPLICATION NUMBER: 05/09/852,209A
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/410,349
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/110,749
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/135,426
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 60/144,022
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 345
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-852-209A-3
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Query Match      57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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QY      2 DRLVSIIRTRGQIHS 15
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Db      47 ERLITVSTNGSIHS 60
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RESULT 14
US-09-978-697-488
; Sequence 488, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 488, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferreira, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Garber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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Query Match 57.5%; Score 42; DB 10; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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db 47 ERITVSTNGSIHS 60

RESULT 16
US-09-999-832A-488
Sequence 488, Application US/09999832A
Publication No. US70020192706N1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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Query Match      57.5%: Score 42; DB 10; Length 345;
                  42.9%: Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY      2 DLVSTSTGSHS 15
DB      47 ERITVSTNSHS 60

RESULT 17
US-09-978-189-488
; Sequence 488, Application US/09978189
; Publication No. US2003004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P63091C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11
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; PRIOR FILING DATE: 1998-03-26
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
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;; PRIOR APPLICATION NUMBER: 60/082704
;; PRIOR FILING DATE: 1998-04-22
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;; PRIOR FILING DATE: 1998-04-23
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;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083392
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083495
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083496
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083499
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;; PRIOR APPLICATION NUMBER: 60/083500
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;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
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;; PRIOR APPLICATION NUMBER: 60/084600
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;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
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;; PRIOR FILING DATE: 1998-05-13
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704

;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
Query Match 57.5%; Score 42; DB 11; Length 345;
Best local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DRVSIRTRGQHS 15
Db 47 ERITVSTNGSIHS 60
RESULT 18
US-09-796-753-6
; Sequence 6, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
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; PRIOR FILING DATE: 1999-12-29
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; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751

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; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 6
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-6

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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 2 DRVSIRTRGOIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

```

```

RESULT 19
US-09-978-608A-488

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```

; Sequence 488, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See file wrapper or Palm
; SEQ ID NO 488
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-488

```

```

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 2 DRVSIRTRGOIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

```

```

RESULT 20
US-09-978-585A-488

```

```

; Sequence 488, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See file wrapper or Palm
; SEQ ID NO 488
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-488

```

```

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

```

OY 2 DRVSIRTRGOIHS 15
:|:::| | | | |
Db 47 ERITVSTNGSIHS 60

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RESULT 21
US-09-978-191A-488

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; Sequence 488, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

```

APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
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PRIOR APPLICATION NUMBER: 60/079663
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
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PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
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PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06

| | | | | |
|--------------------------|-----------------|-----------|--------|-----------------|
| Prior Application Number | | | | |
| Query Match | 57.58; | Score | 42; DB | 11; Length 345; |
| Best Local Similarity | 42.98; | Pred. No. | 11; | |
| Mismatches | 6; Conservative | Indels | 3; | Gaps |
| | | | | 0; |

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OY      2 DRVYSTRTGQIHS 15
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Db      47 ERITVSTNGSIHS 60

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1  RESULT: 22
2  US-09-978-403A-488
3  Sequence 488, Application US/09978403A
4  Publication No. US20030052040A1
5
6  GENERAL INFORMATION:
7  APPLICANT: Ashkenazi, Avi
8  APPLICANT: Baker Kevin P.
9  APPLICANT: Bostein, David
10 APPLICANT: Desnoyers, Luc
11 APPLICANT: Eaton, Dan
12 APPLICANT: Ferrara, Napoleon
13 APPLICANT: Filvaroff, Ellen
14 APPLICANT: Fong, Sherman
15 APPLICANT: Gao, Wei-Qiang
16 APPLICANT: Gerber, Hanspeter
17 APPLICANT: Geritsen, Mary E.
18 APPLICANT: Goddard, Andre J.
19 APPLICANT: Godowski, Paul J.
20 APPLICANT: Grunwald, J. Christopher
21 APPLICANT: Guiney, Austin L.
22 APPLICANT: Hillan, Kenneth J.
23 APPLICANT: Kiljavan, Iyas S.
24 APPLICANT: Kuo, Sophia S.
25 APPLICANT: Napier, Mary A.
26 APPLICANT: Pan, James
27 APPLICANT: Paoni, Nicholas F.
28 APPLICANT: Roy, Margaret Ann
29 APPLICANT: Shelton, David L.

```

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel P.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: F2630P/C17
FILE REFERENCE: A646 Encoding the Same
CURRENT FILING DATE: 2002-03-11
CURRENT FILING DATE: 09/9/18585
PRIOR APPLICATION NUMBER: 60/0762250
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRQIHS 15
Db 47 ERITVSTNGSIHS 60

RESULT 23
US-09-978-564A-488
Sequence 488, Application US/09978564A
Publication No. US2003050241A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlan, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C25

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| 15 | PRIOR APPLICATION NUMBER: 60/077632 | 15 | PRIOR FILING DATE: 1998-04-15 |
| 16 | PRIOR FILING DATE: 1998-03-11 | 16 | PRIOR APPLICATION NUMBER: 60/082568 |
| 17 | PRIOR APPLICATION NUMBER: 60/077641 | 17 | PRIOR FILING DATE: 1998-04-21 |
| 18 | PRIOR FILING DATE: 1998-03-11 | 18 | PRIOR APPLICATION NUMBER: 60/082569 |
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| 20 | PRIOR FILING DATE: 1998-03-11 | 20 | PRIOR APPLICATION NUMBER: 60/082704 |
| 21 | PRIOR APPLICATION NUMBER: 60/077791 | 21 | PRIOR FILING DATE: 1998-04-22 |
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| 60 | PRIOR FILING DATE: 1998-04-01 | 60 | PRIOR APPLICATION NUMBER: 60/084637 |
| 61 | PRIOR APPLICATION NUMBER: 60/080328 | 61 | PRIOR FILING DATE: 1998-05-07 |
| 62 | PRIOR FILING DATE: 1998-04-01 | 62 | PRIOR APPLICATION NUMBER: 60/084639 |
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 2 DRLVSIRTRGOIHS 15
: : : : :
Db 47 ERITVSTNGSIHS 60

RESULT 24
US-09-999-833A-488

Sequence 488, Application US/09999833A
Publication No. US20030054405A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC65
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-15

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21 PRIOR APPLICATION NUMBER: 60/082796
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Query Match      57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      2 DRAVSIRTRQIHS 15
DB      47 ERITVSTNGSIHS 60

RESULT 26
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; Publication No. US2003055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978, 824
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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 2 DRLVSRTRGQHS 15
Db 47 ERITVSTNGSIHS 60
RESULT 27
US-09-918-585A-488
; Sequence 488, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Fonzy, Sherman
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C1
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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

0Y 2 DRVSIRTRGOIHS 15
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Db 47 ERITVSTNGSIHS 60

RESULT 28
US-09-978-423A-488
Sequence 488, Application US/09978423A
Publication No. US20030069178A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavich, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunnas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC21
CURRENT APPLICATION NUMBER: US/09/978, 423A
CURRENT FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Query Match 57.5%; Score 42; DB 11; Length 345;
Best Local Similarity 42.9%; Pred. NO. 11;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Db 47 ERITVSYNGSIHS 60

RESULT 29
US-09-978-193A-488
; Sequence 488, Application US/09978193A
; Publication No. US20030073624A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fon9, Sherman
; APPLICANT: Geo, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; PRIOR FILING DATE: 2002-02-21
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Query Match 57.5%; Score 42; DB 11; Length 345;
 Best Local Similarity 42.9%; Pred. No. 11;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVSIRTRGQIHS 15
 Db 47 ERITVSTNGSIHS 60

RESULT 30
 US-09-999-830A-488
 ; Sequence 488, Application US/09999830A
 ; Publication No. US20030077700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geo, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gutney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C70
CURRENT APPLICATION NUMBER: US/09/999,830A
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match

57.5%; Score 42; DB 11; Length 345;

Best Local Similarity 42.9%; Pred. No. 11;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 2 DRLVSRTRGOIHS 15
: : : : : | | | | |
DB 47 ERITVSTNGSIHS 60

Search completed: August 29, 2003, 18:47:45
Job time : 26.5714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 15.4286 Seconds

(without alignments)
93.497 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

Sequence: 1 IDRLVSIIRGQIHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 58 | 79.5 | 429 | 1 JE0406 | alpha-amylase (BC |
| 2 | 54 | 74.0 | 153 | 2 A21826 | alpha-amylase (BC |
| 3 | 54 | 74.0 | 427 | 1 ALBHB | alpha-amylase (BC |
| 4 | 51 | 69.9 | 135 | 2 C21826 | alpha-amylase (BC |
| 5 | 45 | 61.6 | 365 | 2 A69593 | marlengenin-chalcon |
| 6 | 45 | 61.6 | 428 | 2 S10013 | alpha-amylase (BC |
| 7 | 45 | 61.6 | 434 | 2 S12775 | alpha-amylase (BC |
| 8 | 44 | 60.3 | 458 | 2 G86601 | coproporphyrinogen |
| 9 | 44 | 60.3 | 458 | 2 E72023 | oxygen-independent |
| 10 | 42 | 57.5 | 151 | 2 D87683 | conserved hypotnet |
| 11 | 42 | 57.5 | 166 | 2 C90464 | hypothetical prote |
| 12 | 42 | 54.8 | 141 | 2 AR2812 | 50S ribosomal prot |
| 13 | 40 | 54.8 | 141 | 2 B97591 | 50S ribosomal prot |
| 14 | 40 | 54.8 | 246 | 2 E75481 | RNA methyltransfer |
| 15 | 39 | 53.4 | 443 | 2 S59771 | hypothetical prote |
| 16 | 39 | 53.4 | 445 | 2 A56043 | steroid hormone re |
| 17 | 39 | 53.4 | 446 | 2 I49021 | retinoid X recepto |
| 18 | 39 | 53.4 | 446 | 2 I59354 | orphan nuclear rec |
| 19 | 39 | 53.4 | 447 | 2 I38975 | nuclear orphan rec |
| 20 | 39 | 53.4 | 461 | 2 J04014 | steroid hormone nu |
| 21 | 39 | 53.4 | 585 | 2 S46034 | hypothetical prote |
| 22 | 39 | 53.4 | 585 | 2 S57596 | ribosomal RNA proc |
| 23 | 38 | 52.1 | 1729 | 2 B81407 | ribosomal protein |
| 24 | 38 | 52.1 | 223 | 2 B46537 | hypothetical prote |
| 25 | 38 | 52.1 | 319 | 2 H36792 | hypothetical prote |
| 26 | 38 | 52.1 | 368 | 2 S30409 | hypothetical prote |
| 27 | 37 | 50.7 | 118 | 2 JE0398 | ribosomal protein |
| 28 | 37 | 50.7 | 119 | 2 S77863 | ribosomal protein |
| 29 | 37 | 50.7 | 142 | 2 AH3349 | LSU ribosomal prot |

| | | | | | |
|-----|------|------|------|----------|----------------------|
| 30 | 37 | 50.7 | 251 | 2 J01722 | 3b protein - canin |
| 31 | 37 | 50.7 | 258 | 2 T36303 | probable indolegly |
| 32 | 37 | 50.7 | 283 | 2 S41412 | tetrahydroxynaphth |
| 33 | 37 | 50.7 | 337 | 1 PAPPE | fructose-bisphosph |
| 34 | 37 | 50.7 | 363 | 2 A31342 | fructose-bisphosph |
| 35 | 37 | 50.7 | 383 | 1 ALPCC | alpha-amylase (EC |
| 36 | 37 | 50.7 | 412 | 2 C96789 | protein T23218.6 (|
| 37 | 37 | 50.7 | 444 | 2 T50931 | hypothetical prote |
| 38 | 37 | 50.7 | 450 | 2 B70506 | hypothetical prote |
| 39 | 37 | 50.7 | 475 | 2 S34511 | hypothetical prote |
| 40 | 37 | 50.7 | 566 | 2 S64005 | hypothetical prote |
| 41 | 37 | 50.7 | 574 | 2 T16328 | hypothetical prote |
| 42 | 37 | 50.7 | 615 | 2 T49586 | hypothetical prote |
| 43 | 37 | 50.7 | 647 | 2 S56247 | related to nif-spe |
| 44 | 37 | 50.7 | 1804 | 2 T37320 | probable membrane |
| 45 | 37 | 50.7 | 2514 | 2 T37320 | ataxia telangiecta |
| 46 | 37 | 50.7 | 2619 | 2 T24588 | hypothetical prote |
| 47 | 36.5 | 50.0 | 250 | 2 G87404 | ribosomal protein |
| 48 | 36 | 49.3 | 83 | 2 G87393 | acyl carrier prote |
| 49 | 36 | 49.3 | 232 | 2 T51408 | hypothetical prote |
| 50 | 36 | 49.3 | 253 | 2 J02255 | triose-phosphate 1 |
| 51 | 36 | 49.3 | 257 | 2 G72648 | hypothetical prote |
| 52 | 36 | 49.3 | 267 | 2 F22794 | tryptophan synthas |
| 53 | 36 | 49.3 | 283 | 2 T43146 | hypothetical prote |
| 54 | 36 | 49.3 | 292 | 2 D71364 | probable rRNA meth |
| 55 | 36 | 49.3 | 319 | 2 C72406 | 6-phosphofructokin |
| 56 | 36 | 49.3 | 319 | 2 AC1271 | hypothetical prote |
| 57 | 36 | 49.3 | 319 | 2 AE1633 | probable sugar upt |
| 58 | 36 | 49.3 | 331 | 2 C95998 | conserved hypotet |
| 59 | 36 | 49.3 | 353 | 2 D69001 | alpha-amylase (EC |
| 60 | 36 | 49.3 | 438 | 2 S14957 | sulfate adenylyl- |
| 61 | 36 | 49.3 | 511 | 1 S55198 | probable adenylyl- |
| 62 | 36 | 49.3 | 546 | 1 C70393 | hypothetical prote |
| 63 | 36 | 49.3 | 572 | 2 T34658 | hypothetical prote |
| 64 | 36 | 49.3 | 591 | 2 T45713 | hypothetical prote |
| 65 | 36 | 49.3 | 600 | 2 F84129 | probable histidine |
| 66 | 36 | 49.3 | 639 | 2 S20867 | actin-protein precu |
| 67 | 36 | 49.3 | 639 | 2 AE1190 | hypothetical prote |
| 68 | 36 | 49.3 | 640 | 2 B20338 | hypothetical prote |
| 69 | 36 | 49.3 | 749 | 2 B82089 | hypothetical prote |
| 70 | 36 | 49.3 | 1195 | 2 B96015 | mycoerolate synth |
| 71 | 36 | 49.3 | 2110 | 2 B44110 | mycoerolate synth |
| 72 | 36 | 49.3 | 2111 | 2 A70668 | ribosomal protein |
| 73 | 35 | 47.9 | 119 | 1 R58517 | probable general s |
| 74 | 35 | 47.9 | 193 | 2 D75431 | drup-4-dehydroxam |
| 75 | 35 | 47.9 | 207 | 2 H90339 | hypothetical prote |
| 76 | 35 | 47.9 | 222 | 2 T15359 | alcohol dehydrogen |
| 77 | 35 | 47.9 | 272 | 2 T47354 | beta-lactamase (EC |
| 78 | 35 | 47.9 | 298 | 2 A41381 | probable histidine |
| 79 | 35 | 47.9 | 315 | 2 A95412 | fructose-bisphosph |
| 80 | 35 | 47.9 | 337 | 2 S70469 | fructose-bisphosph |
| 81 | 35 | 47.9 | 338 | 2 A46666 | cytochrome D ubiq |
| 82 | 35 | 47.9 | 379 | 2 AF0137 | probable sugar ABC |
| 83 | 35 | 47.9 | 392 | 2 T45204 | 2-nitropropane dio |
| 84 | 35 | 47.9 | 404 | 2 S57178 | hypothetical prote |
| 85 | 35 | 47.9 | 404 | 2 AB1832 | phytone dehydroge |
| 86 | 35 | 47.9 | 532 | 2 JN0084 | SMP2 protein - yea |
| 87 | 35 | 47.9 | 862 | 2 S30911 | disac-large tumor |
| 88 | 35 | 47.9 | 960 | 1 A39651 | transmembrane prot |
| 89 | 35 | 47.9 | 1259 | 2 JC5523 | acetyl-CoA carboxy |
| 90 | 35 | 47.9 | 2311 | 2 T06161 | cyclic beta 1-2 gl |
| 91 | 35 | 47.9 | 2325 | 2 T02235 | cellulobiose-phospho |
| 92 | 35 | 47.9 | 2831 | 2 T31419 | hypothetical prote |
| 93 | 35 | 47.9 | 2867 | 2 AC3481 | ribosomal protein |
| 94 | 34.5 | 47.3 | 814 | 1 F32223 | ribosomal protein |
| 95 | 34 | 46.6 | 120 | 2 T44411 | ribosomal protein |
| 96 | 34 | 46.6 | 120 | 2 H93027 | 50S ribosomal prot |
| 97 | 34 | 46.6 | 128 | 2 H93027 | hypothetical prote |
| 98 | 34 | 46.6 | 128 | 2 H93027 | conserved hypotet |
| 99 | 34 | 46.6 | 153 | 2 S73561 | |
| 100 | 34 | 46.6 | 159 | 2 E81726 | |

ALIGNMENTS

RESULT 1
JE0406
alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Hordeum vulgare (barley)
C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999
C:Accession: JE0406; B30759; S06275; B31960; B21826
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reek, G.R.; Chandra, G.R.; Muthukrishnan
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-P
A:Reference number: JE0405
A:Accession: JE0406
A:Molecule type: DNA
A:Residues: 1-429 <RAH>
A:Cross-references: EMBL:X15227; NID:918899; PIDN:CAA33299.1; PID:g295805
A:Experimental source: gene Amy56 for alpha-amylase
A:Genetics: A36
R:Rogers, J.C.
submitted to GenBank, September 1988
A:Accession: B30759
A:Reference number: A94535
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-104, 'G', 106-154, 'A', 156-160, 'PD', 163, 'G', 167-196, 'V', 198-342, 'T', 344-392, '
A:Cross-references: GB:J04202; NID:9166984; PIDN:AAA98615.1; PID:g166985
A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B
A:Genetics: A46
R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
Plant Mol. Biol. 9, 3-17, 1987
A:Title: Structure and organization of two divergent alpha-amylase genes from barley.
A:Reference number: S06275
A:Accession: S06275
A:Molecule type: DNA
A:Residues: 1-11, 'LI', 14-32, 'S', 34-57, 'I', 59-79, 'Y', 81-139, 'R', 141-160, 'PA', 163-164, 'R', '
A:Cross-references: EMBL:M7125; NID:9166978; PIDN:AAA2926.1; PID:g166979
A:Experimental source: cv. Sundana gene for alpha-amylase 1 precursor (clone p141.117)
A:Genetics: A41
A>Note: the authors translated the codon TCG for residue 33 as Trp
R:Khurshed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
A:Title: Barley alpha amylase genes. Quantitative comparison of steady-state mRNA levels
A:Reference number: A92700; MUID:8906691; PMID:3264283
A:Accession: B31960
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-51 <KHD>
A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor
R:Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S.
J. Mol. Appl. Genet. 2, 579-588, 1984
A:Reference number: A92837; MUID:85159405; PMID:6335720
A:Accession: B21826
A:Molecule type: mRNA
A:Residues: 379-389, 'T', 391-392, 'D', 394-429 <HUA>
A:Cross-references: GB:K02636; NID:9166992; PIDN:AAA32932.1; PID:g166993
A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)
A:Genetics: <A56>
A:Gene: Amy56
A:Introns: 29/3; 346/3
C:Genetics: <A46>
A:Gene: Amy46
C:Genetics: <AA1>
A:Gene: Amy1
A:Map position: 6
A:Introns: 29/3; 346/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; germination; glycosidase; hydrolase; polysaccharide degradati
F:172-318/Domain: alpha-amylase core homology <AMY>

F:205,230,315/Active site: Asp, Glu, Asp #status predicted

Query Match 79.5%; Score 58; DB 1; Length 429;
Best Local Similarity 86.7%; Pred. No. 0.0062;
Matches 13; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIIRFGQIHS 15
DB 360 IDRLVSIIRFGQIHS 374
|||||
|||||

RESULT 2

A21826
alpha-amylase (EC 3.2.1.1) (clone 103) - barley (fragment)

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Hordeum vulgare (barley)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 22-Jun-1999

C:Accession: A21826
R:Huang, J.K.; Swegle, M.; Dandekar, A.M.; Muthukrishnan, S.
J. Mol. Appl. Genet. 2, 579-588, 1984
A:Reference number: A92837; MUID:85159405; PMID:6335720
A:Accession: A21826
A:Molecule type: mRNA
A:Residues: 1-153 <HUA>

A:Cross-references: GB:M10056; NID:9166988; PIDN:AAA32930.1; PID:g166989
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; carbohydrate metabolism; germination; glycosidase; hydrola

Query Match 74.0%; Score 54; DB 2; Length 153;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSIIRFGQIHS 15
DB 84 IDRLVSIIRFGQIHS 98
|||||
|||||

RESULT 3

ALBHB
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2
C:Species: Hordeum vulgare (barley)
C>Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999

C:Accession: A31960; A00847; JE0405; A26267; A24457; A30759
R:Khurshed, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA lev
A:Reference number: A92700; MUID:8906691; PMID:3264283
A:Molecule type: DNA
A:Residues: 1-427 <KHD>
A:Cross-references: GB:J04202
A:Experimental source: cv. Himalaya; gene Amy6-4
R:Rogers, J.C.
J. Biol. Chem. 260, 3731-3738, 1985

A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone
A:Reference number: A00847; MUID:85131184; PMID:3871776
A:Accession: A00847
A:Molecule type: mRNA
A:Residues: 1-133, 'D', 135-194, 'HRL', 198-424, 'Q', 426-427 <ROG>

A:Experimental source: seed
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reek, G.R.; Chandra, G.R.; Muthukrishn
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for hig
A:Reference number: JE0405
A:Accession: JE0405
A:Molecule type: DNA
A:Residues: 1-133, 'D', 135-424, 'Q', 426-427 <RAH>

A:Cross-references: EMBL:X15226; NID:918894; PIDN:CAA33298.1; PID:g295804
A:Experimental source: gene Amy152

R.Chandler, P.M.; Zwar, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Inglis, A.S.
 Plant Mol. Biol. 3, 407-418, 1984
 A>Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels
 A:Reference number: A26267
 A:Accession: A26267
 A:Molecule type: mRNA
 A:Residues: 1-133, 'V', 135-184, 'A', 186-366, 'GA' <GNA>
 A:Experimental source: cv. Himalaya
 A:Note: The authors translated the codon GTC for residue 134 as Gly
 R.Svensson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.
 Carlsberg Res. Commun. 50, 15-22, 1985
 A>Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.
 A:Reference number: A24457
 A:Accession: A24457
 A:Molecule type: Protein
 A:Residues: 25-59, 'X', 61-67, 'HX', 70-85, 'X', 87-92, 'E', 94, 146-165; 228-251; 297-303, 'X', 305-
 C:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated al-
 ed by the embryo during germination.
 C:Genetics:
 A:Gene: Amy2-2
 A:Map position: 6
 A:Introns: 29/3, 344/3
 A:Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-am-
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosidase;
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-427/Product: alpha-amylase #status experimental <AMT>
 F:170-316/Domain: alpha-amylase core homology <AMY>
 F:25/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carb
 F:203,228,313/Active site: Asp, Glu, Asp #status predicted

Query Match 74.0%; Score 54; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.035;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 15
 |||||:||||
 DB 358 IDRLVSIRTRGQIHN 372

RESULT 4
 C21826
 alpha-amylase (EC 3.2.1.1) (clone 168) - barley (fragment)
 M:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: Hordeum vulgare (barley)
 C>Date: 05-Jun-1997 #sequence_revision 05-Jun-1987 #text_change 22-Jun-1999
 C:Accession: C21826
 R: Huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muchukrishnan, S.
 J. Mol. Appl. Genet. 2, 579-588, 1984
 A:Reference number: A92837; MUID:85159405; PMID:6335720
 A:Accession: C21826
 A:Molecule type: mRNA
 A:Residues: 1-135 <HDA>
 A:CROSS-references: GB:R02635; NID:g166990; PIDN:AAA32931.1; PID:g166991
 C:Comment: The authors translated the codon CAA for residue 47 as Pro and the codon GGG
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; carbohydrate metabolism; germination; glycosidase; hydrolyase;
 F:170-317/Domain: alpha-amylase core homology <AMY>

- Query Match 69.9%; Score 51; DB 2; Length 135;
 Best Local Similarity 73.3%; Pred. No. 0.035;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 15
 |||||:||||
 DB 66 IDRLVSIRTRGQIHS 80

RESULT 5
 A69593
 naringenin-chalcone synthase bcsa - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: A69593
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C: Bron, S.; Broutillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A: Ehrlich, S.D.; Emerson, P.T.; Entlian, K.D.; Errington, J.; Faure, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Follmer, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal-
 lech, J.; Harwood, C.R.; Henuat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koester, P.; Konungstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapius, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 Y, M.; Ogawa, K.; Ogawa, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scani
 A:Authors: Schleich, S.; Schrotter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
 akuchl, M.; Tamakoshi, A.; Tanaka, T.; Terpieta, P.; Tognoni, A.; Tosato, V.; Uchida
 T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: A69593
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-365 <XUN>
 A:CROSS-references: GB:299115; GB:AL009126; NID:g2634478; PIDN:CAB14122.1; PID:g26346
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: bcsa
 C:Superfamily: chalcone synthase

Query Match 61.6%; Score 45; DB 2; Length 365;
 Best Local Similarity 66.7%; Pred. No. 1.5;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 15
 |||||:||||
 DB 36 IDRLVSIRTRGQIHS 50

RESULT 6
 S10013
 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-O5g2) - rice
 C:Species: Oryza sativa (rice)
 C>Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R: Huang, N.; Sutcliffe, T.D.; Litts, J.C.; Rodriguez, R.L.
 Plant Mol. Biol. 14, 655-668, 1990
 A>Title: Classification and characterization of the rice alpha-amylase multigene fami
 A:Reference number: S10013; MUID:91346577; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HDA>
 A:CROSS-references: EMBL:X16509; NID:g20166; PIDN:CAA34516.1; PID:g20167
 A:Experimental source: var. M202
 C:Genetics:
 A:Introns: 30/3; 75/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMY>

- Query Match 61.6%; Score 45; DB 2; Length 428;
 Best Local Similarity 71.4%; Pred. No. 1.8;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 14
 |||||:||||
 DB 359 IDRLVSIRTRGQIHS 372

```
RESULT 7
S12775
alpha-amylase (EC 3.2.1.1) precursor (clone pos103) - rice
C:Species: Oryza sativa (rice)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: S12775
R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
Mol. Gen. Genet. 221, 235-244, 1990
A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and m
A:Reference number: S12775; MUID:90318322; PMID:2370848
A:Accession: S12775
A:Molecule type: mRNA
A:Residues: 1-434 <ONE>
A:Cross-references: EMBL:M24286; NID:9169752; PIDN:AAA33885.1; PID:9169753
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:16-333/domain: alpha-amylase core homology <AMY>
F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match 61.6%; Score 45; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 1.8;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
|:|||||:|
Db 365 IERLVSIRTRGOIH 378

RESULT 8
G86601
coproporphyrinogen III oxidase [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G86601
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: G86601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <STO>
A:Cross-references: GB:BA000008; NID:98979263; PIDN:BAAG9097.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: hemm_2
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 60.3%; Score 44; DB 2; Length 458;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
|:|:|:|:|
Db 405 DRLISMETGTLIHN 418

RESULT 9
E72023
oxygen-independent coproporphyrinogen III oxidase CP0977 [imported] - Chlamydomophila pneu
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: E72023; H81517
R:Kaltman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: E72023
A>Status: preliminary
```

```
A:Molecule type: DNA
A:Residues: 1-458 <ARN>
A:Cross-references: GB:AE001669; GB:AE001363; NID:94377199; PIDN:AAD19027.1; PID:9437
A:Experimental source: strain CML029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: H81517
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-458 <REA>
A:Cross-references: GB:AE002256; GB:AE002161; NID:97189893; PIDN:AAF38757.1; PID:9718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: hemm_2; CP0977
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 60.3%; Score 44; DB 2; Length 458;
Best Local Similarity 57.1%; Pred. No. 3;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGOIHS 15
|:|:|:|:|
Db 405 DRLISMETGTLIHN 418

RESULT 10
D87683
conserved hypothetical protein CC3502 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87683
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: AB7249; MUID:21173698; PMID:11259647
A:Accession: D87683
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: GB:AE005673; NID:913425228; PIDN:AAK25464.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3502

Query Match 57.5%; Score 42; DB 2; Length 151;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 9; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 2 DRLVSIRTRTRGTHS 15
|:|:|:|:|
Db 54 DRLVAVETTAARGETIHT 71

RESULT 11
C90464
hypothetical protein acsa-9 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: C90464
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90464
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-666 <KUR>
```

A:Cross-references: GB:AE006641; NID:g13816221; PIDN:AAK42970.1; GSPDB:GN00155
 C:Genetics:
 A:Gene: acsA-9
 C:Superfamily: acetate-CoA ligase; acetate-CoA ligase homology

Query Match 57.5%; Score 42; DB 2; Length 666;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
 ::|||::|::|::|
 DB 19 LMRVLSITTYKEIHS 33

RESULT 12
 AH2812
 50S ribosomal protein L17 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AH2812
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 ; Karp, G.; Gallet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH2812
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141 <KUN>
 A:Cross-references: GB:AE008688; PIDN:AAL42918.1; PID:g17740374; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: rplO
 A:Map position: circular chromosome
 C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 54.8%; Score 40; DB 2; Length 141;
 Best Local Similarity 40.0%; Pred. No. 4.6;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
 ::|||::|::|::|
 DB 48 VERLVTLGKRQDLHA 62

RESULT 13
 B97591
 50S ribosomal protein L17 nma0102 [imported] - Agrobacterium tumefaciens (strain C58, Ce
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: B97591
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wolim, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: AB7359; MUID:21608551; PMID:11743194
 A:Accession: B97591
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-141 <KUN>
 A:Cross-references: GB:AE007869; PIDN:AAK87683.1; PID:g15157042; GSPDB:GN00169
 C:Genetics:
 A:Gene: ACR_C_3516
 A:Map position: circular chromosome
 C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 54.8%; Score 40; DB 2; Length 141;
 Best Local Similarity 40.0%; Pred. No. 4.6;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 15
 ::|||::|::|::|
 DB 48 VERLVTLGKRQDLHA 62

RESULT 14
 E75481
 RNA methyltransferase, TrmH family - Deinococcus radiodurans (strain RI)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: E75481
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
 ; Shen, M.; Yamathavan, J.; Lam, P.; McDonald, D.; Uterback, T.; Zaleski, C.;
 ; Smith, H.; Yoder, T.; Yoder, C.; Fraser, C.M.
 Science 266, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75481
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <MHL>
 A:Cross-references: GB:AE001930; GB:AE000513; NID:g6458450; PIDN:AAF10325.1; PID:g6445
 A:Experimental source: strain RI
 C:Genetics:
 A:Gene: DR0748
 A:Map position: 1
 C:Superfamily: conserved hypothetical protein H10860

Query Match 54.8%; Score 40; DB 2; Length 246;
 Best Local Similarity 64.3%; Pred. No. 8.5;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 DRLVSIRTRGQIHS 15
 |||||::|::|::|
 DB 208 DVLVSIPVRGQVOS 221

RESULT 15
 S59771
 hypothetical protein YPR106w - Yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein P8283.9
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998
 C:Accession: S59771
 R:Nelson, J.
 submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of S. cerevisiae cosmid 8283.
 A:Reference number: S59764
 A:Accession: S59771
 A:Molecule type: DNA
 A:Residues: 1-443 <NEL>
 A:Cross-references: EMBL:U32445; NID:g914969; PID:g914977; MIPS:YPR106w
 C:Genetics:
 A:Gene: SGD:ISR1
 A:Cross-references: SGD:S0006310; MIPS:YPR106w
 A:Map position: 16R

Query Match 53.4%; Score 39; DB 2; Length 443;
 Best Local Similarity 57.1%; Pred. No. 25;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGQIHS 14
 |||||::|::|::|
 DB 265 IDALKSLKTKNGIHH 278

RESULT 16
 A56043
 steroid hormone receptor-like protein RUD-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999
 C:Accession: A56043
 R:Apfel, R.; Bendbrook, D.; Bernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfahl, M.

Mol. Cell. Biol. 14, 7025-7035, 1994
A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive elements
A:Reference number: A56043; MUID:95021230; PMID:7935418
A:Accession: A56043
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <RES>
A:Cross-references: GB:011685; NID:9555751; PIDN:AAA53633.1; PID:9555752
A:Note: authors translated the codon GAG for residue 73 as Ser
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: steroid hormone receptor; zinc finger
F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 445;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
Db 409 KLVSLRTLSSVHS 421

RESULT 17
retinoid X receptor interacting protein No.15 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49021
R:Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-85, 1995
A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:
A:Reference number: A57664; MUID:95280959; PMID:7760852
A:Accession: I49021
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-446 <RES>
A:Cross-references: EMBL:U09419; NID:9691713; PIDN:AA52164.1; PID:9691714
C:Genetics:
A:Gene: R1P15
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 446;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
Db 409 KLVSLRTLSSVHS 421

RESULT 18
orphan nuclear receptor OR-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I59354; I59264
R:Teouli, M.; Enmark, E.; Li, Q.; Wikstrom, A.C.; Peltto-Huikko, M.; Gustafsson, J.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 2096-2100, 1995
A:Title: OR-1, a member of the nuclear receptor superfamily that interacts with the 9-cis
A:Reference number: I59354; MUID:95199298; PMID:7892230
A:Accession: I59354
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-446 <RES>
A:Cross-references: EMBL:U20389; NID:9665941; PIDN:AAA69522.1; PID:9665942
A:Experimental source: Sprague-Dawley, hepatic
R:Song, C.; Kokontis, J.M.; Hilpakka, R.A.; Liao, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 10809-10813, 1994
A:Title: Ubiquitous receptor: a receptor that modulates gene activation by retinoic acid
A:Reference number: I59264; MUID:95062154; PMID:7971966
A:Accession: I59264

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-32, 'V', 34-51, 55-218, 'V', 220-446 <RES2>
A:Cross-references: EMBL:U14533; NID:9565661; PIDN:AAA52361.1; PID:9565662
A:Experimental source: Vagina
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; zinc finger
F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 446;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
Db 409 KLVSLRTLSSVHS 421

RESULT 19
I38975
nuclear orphan receptor LXR-alpha - human
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Sep-1999
C:Accession: I38975
R:Killy, P.J.; Unesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
Genes Dev. 9, 1033-1045, 1995
A:Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
A:Reference number: I38975; MUID:95262897; PMID:7744246
A:Accession: I38975
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-447 <RES>
A:Cross-references: EMBL:U22662; NID:9726512; PIDN:AA85856.1; PID:9726513
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:96-367/Domain: erba transforming protein homology <ERBA>

Query Match 53.4%; Score 39; DB 2; Length 447;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
Db 410 KLVSLRTLSSVHS 422

RESULT 20
JC4014
steroid hormone-nuclear receptor NER - human
C:Species: Homo sapiens (man)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
C:Accession: JC4014
R:Shinar, D.M.; Endo, N.; Rutledge, S.T.; Vogel, R.; Rodan, G.A.; Schmidt, A.
Gene 147, 273-276, 1994
A:Title: NER, a new member of the gene family encoding the human steroid hormone nucl
A:Reference number: JC4014; MUID:95011628; PMID:7926814
A:Accession: JC4014
A:Molecule type: mRNA
A:Residues: 1-461 <SHI>
A:Cross-references: GB:U07132; NID:9641961; PIDN:AAA61783.1; PID:9641962
A:Experimental source: osteosarcoma cells SAOS-2/810
C:Genetics:
A:Gene: GDB:UNR
A:Cross-references: GDB:389570; OMIM:600380
A:Map position: 19q13.3-19q13.3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: steroid hormone receptor
F:85-381/Domain: erba transforming protein homology <ERBA>
F:87-154/Domain: DNA binding; status predicted <BIN>

Query Match 53.4%; Score 39; DB 2; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 15
 :||||:|:|:|
 Db 424 KLVSLRLLSVHS 436

RESULT 21

S46034
 Hypothetical protein YBR163w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YBR1215
 C:Species: Saccharomyces cerevisiae
 C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
 C:Accession: S46034
 R:Enlilan, K.D.; Koeltter, P.; Rose, M.; Becker, J.; Grey, M.; Li, Z.; Niegemann, E.; Sche
 S.; Gruenbein, R.; Helges, D.; Klesau, P.; Korol, S.; Krems, B.; Proft, M.; Slegers, K.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S46034
 A:Accession: S46034
 A:Molecule type: DNA
 A:Residues: 1-185 <ENT>
 A:Cross-references: EMBL:Z36032; NID:G536499; PID:G536500; GSPDB:GN00002; MIPS:YBR163w
 A:Experimental source: strain S288C
 C:Gene: SCD; DML: MIPS:YBR163w
 A:Cross-references: SGD:S0000367
 A:Map position: 2R
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YBR163w

Query Match 53.4%; Score 39; DB 2; Length 585;
 Best Local Similarity 53.3%; Pred. No. 34;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
 :||||:|:|:|
 Db 218 INRLVSLFTKGDGHA 232

RESULT 22

S57596
 Ribosomal RNA processing protein RRP5 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YM9959.11c; protein YMR229c
 C:Species: Saccharomyces cerevisiae
 C>Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
 C:Accession: S57596; S72446
 R:Skellton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: S57587
 A:Accession: S57596
 A:Molecule type: DNA
 A:Residues: 1-1729 <SMK>
 A:Cross-references: EMBL:Z49939; NID:G887599; PIDN:CAA90200.1; PID:G887610; MIPS:YMR229c
 A:Experimental source: strain AB972
 R:Venema, J.; Tollervey, D.
 EMBO J. 15, 5701-5714, 1996
 A:Title: RRP5 is required for formation of both 18S and 5.8S rRNA in yeast.
 A:Reference number: S72446; MUID:97051828; PMID:8896463
 A:Accession: S72446
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-1729 <VEN>
 A:Cross-references: EMBL:Z49939; NID:G887599; PIDN:CAA90200.1; PID:G887610
 C:Gene: SCD; FMI: MIPS:YMR229c
 A:Cross-references: SGD:S0004842; MIPS:YMR229c
 C:Map position: 13R
 C:Function:
 A:Description: required for pre-rRNA processing
 C:Superfamily: ribosomal RNA processing protein RRP5
 C:Keywords: nucleus; RNA binding

Query Match 53.4%; Score 39; DB 2; Length 1729;
 Best Local Similarity 41.7%; Pred. No. 11e+02;
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 RLVSIRTRGOIHS 14
 :||||:|:|:|
 Db 565 RLVSINRGNVH 576

RESULT 23

B87407
 ribosomal protein L17 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: B87407
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, R.; Nierman, W.C.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Ko
 n, J.; Ermolaeva, M.; White, O.; S.A. 98 4136-4141, 2001
 Proc. Natl. Acad. Sci. U.S.A. 98 4136-4141, 2001
 A:Title: Complete genome sequence of Caulobacter crescentus.
 A:Reference number: B87407; MUID:21173698; PMID:11259647
 A:Accession: B87407
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-137 <SMO>
 A:Cross-references: GB:AE005673; NID:G1342606; PIDN:AAK23254.1; GSPDB:GN00148
 C:Gene: CCL273
 C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 52.1%; Score 38; DB 2; Length 137;
 Best Local Similarity 33.3%; Pred. No. 11;
 Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
 :||||:|:|:|
 Db 48 VEVLYTLAKRGDLHA 62

RESULT 24

S48937
 Hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 29-Oct-1999
 C:Accession: S48937
 R:Pavellio, T.
 submitted to the EMBL Data Library, June 1994
 A:Description: The sequence of S. cerevisiae cosmid 9196.
 A:Reference number: S46794
 A:Accession: S48937
 A:Molecule type: DNA
 A:Residues: 1-223 <FAV>
 A:Cross-references: EMBL:U11583; NID:G2289854; PIDN:AA65043.1; PID:G2289860; MIPS:YH
 C:Gene: SCD; GOS1
 A:Cross-references: SGD:S0001023; MIPS:YHL031c
 A:Map position: 8L

Query Match 52.1%; Score 38; DB 2; Length 223;
 Best Local Similarity 52.9%; Pred. No. 18;
 Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 1 IDRLVSIRTRGOIHS 15
 :||||:|:|:|
 Db 152 VDRLSQAMETRSOPHS 168

RESULT 25

H36792
 Hypothetical protein ORF61 - Ictalurid herpesvirus 1 (strain Auburn 1)
 C:Species: Ictalurid herpesvirus 1
 A:Note: host Ictalurus punctatus (channel catfish)
 C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
 C:Accession: H36792
 R:Davidson, A.J.
 submitted to Genbank, January 1992

A:Description: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A36804
 A:Accession: H36792
 A:Molecule type: DNA
 A:Residues: 1-319 <DNA>
 A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA88164.1; PID:g331271
 R:Davidson, A.U.
 Virology 186, 9-14, 1992
 A:Title: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A39447; MUID:92087490; PMID:1727613
 A:Contents: annotation
 A:Note: neither protein nor nucleic acid sequence is given
 C:Genetics:
 A:Gene: 61

Query Match 52.1%; Score 38; DB 2; Length 319;
 Best Local Similarity 46.2%; Pred. No. 27;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIIRTCOI 13
 :||| :|||:
 Db 213 VDRGLKLRAGEV 225

RESULT 26
 S50409
 hypothetical protein YMR152w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YMR520.01; hypothetical protein YMR375.22
 C:Species: Saccharomyces cerevisiae
 C:Date: 27-Jan-1995 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
 C:Accession: S50409; S16819; S54510; S54597
 R:Badcock, K.; Churcher, C.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S50388
 A:Accession: S50409
 A:Molecule type: DNA
 A:Residues: 1-316 <BAD>
 A:Cross-references: EMBL:Z47071; NID:9606429; PIDN:CAA87367.1; PID:9606451; MIPS:YMR152w
 R:Behrens, M.; Michaelis, G.; Pratlje, E.
 Mol. Gen. Genet. 228, 167-176, 1991
 A:Title: Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae shows sequence
 A:Reference number: S16817; MUID:91360060; PMID:1886606
 A:Accession: S16819
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-120, 'T', 122-233, 'T', 235-279, 'N', 281-295, 'S', 297-365 <BEH>
 R:Hunt, S.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54510
 A:Accession: S54510
 A:Molecule type: DNA
 A:Residues: 196-365 <HUN>
 A:Cross-references: GB:Z49705; EMBL:Z49700; NID:9825556; PIDN:CAA89788.1; PID:9825557; EMBL:Z49705
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD:YIM1
 A:Cross-references: SGD:S0004760
 A:Map position: 13R
 C:Keywords: transmembrane protein
 F:170-186/Domain: transmembrane #status predicted <TMM>

Query Match 52.1%; Score 38; DB 2; Length 365;
 Best Local Similarity 53.8%; Pred. No. 32;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIIRTCOI 13
 :|||:| :|||:
 Db 348 IDRLMSNRAGKV 360

RESULT 27
 JE0398
 ribosomal protein L17 - Thermus aquaticus (strain HB8)

C:Species: Thermus aquaticus
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
 C:Accession: JE0398
 R:Wada, T.; Yamazaki, T.; Kuramitsu, S.; Kyogoku, Y.
 J. Biochem. 125, 143-150, 1999
 A:Title: Cloning of the RNA polymerase alpha subunit gene from Thermus thermophilus H
 A:Reference number: JE0397; MUID:99098837; PMID:9880810
 A:Accession: JE0398
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-118 <WAD>
 C:Genetics:
 A:Gene: rpl17
 C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 50.7%; Score 37; DB 2; Length 118;
 Best Local Similarity 33.3%; Pred. No. 14;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 IDRLVSIIRTCOIH 15
 :||| :|||:
 Db 48 VDHLIHLAKRGDLHA 62

RESULT 28
 S77863
 ribosomal protein L17 - Mycoplasma capricolum (fragment)
 N:Alternate names: protein MC060
 C:Species: Mycoplasma capricolum
 C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
 C:Accession: S77863; S48596
 R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, M.; Microbiol. 16, 955-967, 1995
 A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology
 A:Reference number: S77739; MUID:96059641; PMID:7476192
 A:Accession: S77863
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-119 <BOR>
 A:Cross-references: EMBL:Z33050; NID:9541697; PIDN:CAA83721.1; PID:94379134
 A:Experimental source: ATCC 27343
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: Escherichia coli ribosomal protein L17
 C:Keywords: protein biosynthesis; ribosome

Query Match 50.7%; Score 37; DB 2; Length 119;
 Best Local Similarity 35.7%; Pred. No. 14;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 2 DRLVSIIRTCOIH 15
 :||| :|||:
 Db 46 DHMITLAKRGDLHS 59

RESULT 29
 AH3349
 LSU ribosomal protein L17P [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C:Accession: AH3349
 R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mufer, C.; Los, T.; Ivanov, I.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756888
 A:Accession: AH3349
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-142 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL51963.1; PID:917982722; GSPDB:GN00190
 A:Experimental source: strain 16M

C:Genetics:
A:Gene: BME10782
A:Map position: I
C:Superfamily: Escherichia coli ribosomal protein L17

Query Match 50.7%; Score 37; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 17;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIIRGQIHS 15
:::|::|::|:
Db 48 VEKLVTLGKRGDLHA 62

RESULT 30

J01722
3b:protein - canine coronavirus
C:Species: canine coronavirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: J01722
R:Horshburgh, B.C.; Brierley, I.; Brown, T.D.K.
J. Gen. Virol. 73, 2849-2862, 1992
A:Title: Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus genomic RNA
A:Reference number: PQ0481; NCID:93057357; PMID:1431811
A:Accession: J01722
A:Molecule type: mRNA
A:Residues: 1-251 <HOR>
A:Cross-references: DDBJ:DJ3096
A:Experimental source: strain insavc-1

Query Match 50.7%; Score 37; DB 2; Length 251;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 LVSIIRGQIHS 15
||| ||| |:
Db 179 LVSIIRGLAHA 190

Search completed: August 29, 2003, 18:48:28
Job time : 17.4286 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 29, 2003, 18:39:11 ; Search time 9.85714 Seconds

(without alignments)
71.562 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73

Sequence: 1 IDRLVSRIRGQIHS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_41.*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 58 | 79.5 | 429 | 1 | AMT6_HORVU |
| 2 | 54 | 74.0 | 427 | 1 | AMT2_HORVU |
| 3 | 54 | 74.0 | 427 | 1 | AMT2_HORVU |
| 4 | 51 | 69.9 | 135 | 1 | AMT5_HORVU |
| 5 | 45 | 61.6 | 365 | 1 | BCSA_BACSU |
| 6 | 45 | 61.6 | 428 | 1 | AMT1_ORYSA |
| 7 | 40 | 54.8 | 368 | 1 | AMT3_HORVU |
| 8 | 39 | 53.4 | 445 | 1 | NRH3_MOUSE |
| 9 | 39 | 53.4 | 445 | 1 | NRH2_MOUSE |
| 10 | 39 | 53.4 | 446 | 1 | NRH2_MOUSE |
| 11 | 39 | 53.4 | 446 | 1 | NRH2_MOUSE |
| 12 | 39 | 53.4 | 447 | 1 | NRH2_MOUSE |
| 13 | 39 | 53.4 | 461 | 1 | NRH2_HUMAN |
| 14 | 39 | 53.4 | 461 | 1 | NRH2_HUMAN |
| 15 | 39 | 53.4 | 461 | 1 | NRH2_HUMAN |
| 16 | 39 | 53.4 | 461 | 1 | NRH2_HUMAN |
| 17 | 38 | 52.1 | 319 | 1 | VRG1_HSV1 |
| 18 | 38 | 52.1 | 319 | 1 | VRG1_HSV1 |
| 19 | 37 | 50.7 | 118 | 1 | RL17_THERM |
| 20 | 37 | 50.7 | 119 | 1 | RL17_THERM |
| 21 | 37 | 50.7 | 141 | 1 | RL17_THERM |
| 22 | 37 | 50.7 | 250 | 1 | VNS3_CVCAI |
| 23 | 37 | 50.7 | 258 | 1 | TRC2_STRGO |
| 24 | 37 | 50.7 | 282 | 1 | T4HR_MAGGR |
| 25 | 37 | 50.7 | 311 | 1 | ISPE_CORGL |
| 26 | 37 | 50.7 | 336 | 1 | FLIP_SHEEP |
| 27 | 37 | 50.7 | 337 | 1 | FLIP_PIG |
| 28 | 37 | 50.7 | 362 | 1 | FLIP_PIG |
| 29 | 37 | 50.7 | 383 | 1 | AMC1_ORYSA |
| 30 | 37 | 50.7 | 475 | 1 | YMA8_YEAST |
| 31 | 37 | 50.7 | 566 | 1 | YMA8_YEAST |
| 32 | 37 | 50.7 | 566 | 1 | YMA8_YEAST |
| 33 | 36.5 | 50.0 | 1604 | 1 | YMA8_YEAST |
| | | | 230 | 1 | RS1_CAUCH |

| | | | | | | | |
|-----|----|------|-----|---|-------------|--------|-------------|
| 34 | 36 | 49.3 | 253 | 1 | TPIS_ORYSA | P48494 | oryza sativ |
| 35 | 36 | 49.3 | 257 | 1 | PCRB_AREPE | O94975 | bercyprum p |
| 36 | 36 | 49.3 | 267 | 1 | TRP2_BACSU | P07601 | bacillus su |
| 37 | 36 | 49.3 | 274 | 1 | 1ZEL_HERAO | P25260 | herpesotiph |
| 38 | 36 | 49.3 | 319 | 1 | K6PE_LISTIN | O92860 | listeria in |
| 39 | 36 | 49.3 | 319 | 1 | K6PE_LISTIN | O92860 | listeria in |
| 40 | 36 | 49.3 | 319 | 1 | K6PE_LISTIN | O92860 | listeria in |
| 41 | 36 | 49.3 | 319 | 1 | K6PE_LISTIN | O92860 | listeria in |
| 42 | 36 | 49.3 | 353 | 1 | TP6A_METTH | O94952 | thermotoga |
| 43 | 36 | 49.3 | 353 | 1 | TP6A_METTH | O94952 | thermotoga |
| 44 | 36 | 49.3 | 521 | 1 | AM3B_ORYSA | O27089 | methanobact |
| 45 | 36 | 49.3 | 521 | 1 | AM3B_ORYSA | O27089 | methanobact |
| 46 | 36 | 49.3 | 546 | 1 | MET3_YEAST | P08536 | oryza sativ |
| 47 | 36 | 49.3 | 639 | 1 | SATC_AOUAE | O67174 | a probable |
| 48 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 49 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 50 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 51 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 52 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 53 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 54 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 55 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 56 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 57 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 58 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 59 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 60 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 61 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 62 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 63 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 64 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 65 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 66 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 67 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 68 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 69 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 70 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 71 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 72 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 73 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 74 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 75 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 76 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 77 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 78 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 79 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 80 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 81 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 82 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 83 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 84 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 85 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 86 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 87 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 88 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 89 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 90 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 91 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 92 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 93 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 94 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 95 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 96 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 97 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
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| 99 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |
| 100 | 35 | 47.9 | 119 | 1 | MCAS_MYCBO | O02251 | mycobacteri |

ALIGNMENTS

AMY6_HORVU STANDARD: PRT; 429 AA.
 ID AMY6_HORVU P04750;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clones GRAMY56 and 963).
 GN AMY1.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 NC Triticaceae; Hordeum.
 NC NCB1_taxonomy:4513;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE GRAMY56).
 RA Rasmussen R.J., Huang J.-K., Clark K.L., Reek G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley.";
 RT Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBryo.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X15227; CAA33299.1; -;
 DR EMBL: K02636; AAA32932.1; -;
 DR PIR: JEO406; JEO406.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 DR KEGG: K02636; Glycosylase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 47937 MW; 1C924CA6319D5262 CRC64;
 Query Match 79.5%; Score 58; DB 1; Length 429;
 Best Local Similarity 86.7%; Pred. No. 0.0018;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDRLVSVTRRGQIHS 15
 Db 360 IDRLVSVTRRGQIHS 374
 ID AMY4_HORVU STANDARD: PRT; 153 AA.
 AC P04748;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clone 103) (Fragment).
 GN AMY1.4.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 NC Triticaceae; Hordeum.
 NC NCB1_taxonomy:4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBryo.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M10056; AAA32930.1; -;
 DR PIR: A21826; A21826.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR KEGG: K02636; Glycosylase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER 1 1
 FT ACT_SITE 39 39 BY SIMILARITY.
 SQ SEQUENCE 153 AA; 17275 MW; BE5233AE1D65F72 CRC64;
 Query Match 74.0%; Score 54; DB 1; Length 153;
 Best Local Similarity 73.3%; Pred. No. 0.0034;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 IDRLVSVTRRGQIHS 15
 Db 84 IDRLVSVTRRGQIHS 98
 RESULT 3


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FT STRAND 341 345
FT HELIX 346 350
FT TURN 351 351
FT HELIX 355 367
FT TURN 368 369
FT TURN 372 373
FT STRAND 376 382
FT TURN 383 384
FT STRAND 385 390
FT TURN 391 393
FT STRAND 394 398
FT HELIX 405 407
FT STRAND 412 418
FT TURN 419 420
FT STRAND 421 427
SQ SEQUENCE 427 AA; 47355 MM; 957COB1662BF748 CRC64;

Query Match 74.0%; Score 54; DB 1; Length 427;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 15
DB 358 IDRLVSIRTRGQIHS 372

RESULT 4
AMY5_HORVU STANDARD; PRT: 135 AA.
ID AMY5_HORVU
AC P04749;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alpha-amylase type B isozyme (EC 3.2.1.1) (1,4'-alpha-D-glucan
glucanohydrolase) (Clone 168) (Fragment).
GN AMY1.5
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85159405; PubMed=6335720;
RA Huang J.-K., Swegle M., Dandekar A.M., Muthukrishnan S.;
RT "Expression and regulation of alpha-amylase gene family in barley
aleurones."
RL J. Mol. Appl. Genet. 2:579-588(1984).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
ACID, WHICH WITHIN 10 HOURS STIMULATES THE HORNE CELLS COVERING
THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
DEVELOPING PLANT EMBRYO.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
BARLEY.
CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
GIBBERELLIC ACID.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----

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DR EMBL: K02635; AAA32931.1; -.
DR PIR: C21826; C21826.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha.amyl.cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT ACT_SITE 21 21
FT NON_TER 1
SQ SEQUENCE 135 AA; 15140 MM; 947F71F5E13DD2A6 CRC64;

Query Match 69.9%; Score 51; DB 1; Length 135;
Best Local Similarity 73.3%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGQIHS 15
DB 66 IDRLVSIRTRGQIHS 80

RESULT 5
BCSA_BACSU STANDARD; PRT: 365 AA.
ID BCSA_BACSU
AC P54157;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative chalcone synthase (EC 2.3.1.74) (Naringenin-chalcone
synthase).
GN BCSA
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRAIN=168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serrot P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
the sera and kgd loci cloned in a yeast artificial chromosome."
RL Microbiology 142:2005-2016(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX SPRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Danilot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Eutani K.D., Errington J., Fabret C., Ferrari E., Fougere D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasanara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porrolik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Setiguchi J., Sekowska A., Serot S.J., Serrot P., Shin B.S., Solado B.,
RA Sorokin A., Tacomoni E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takemoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarcoti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,

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RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-27 FROM N.A.
RC STRAIN-168;
RA Saxild H.H., Christensen L., Nygaard P., Schou S.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 3 malonyl-CoA + 4 coumaroyl-CoA = 4 CoA +
CC naringenin-chalcone + 3 CO(2)
CC
CC -1- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L77246; AAA96613.1; -
CC EMBL: Z99115; CAB14122.1; -
CC PIR: A69593; A69593;
CC DR EMBL; X83878; -; NOT_ANNOTATED_CDS.
CC DR PIR; A69593; A69593.
CC DR Subtilisin; BG11523; bcsA.
CC DR InterPro: IPR001099; N-C-synthase.
CC DR Pfam: PF00195; Chal_still_synth; 1.
CC DR Pfam: PF02797; Chal_still_synth; 1.
CC DR PRODOM: PD000453; N-C-synthase; 1.
CC DR PROSITE: PS00441; CHALCONE_SYNTH; 1.
CC DR Transferase; Acyltransferase; Complete proteome.
CC KM ACT SITE 144 144 BY SIMILARITY.
CC FT ACT SITE 144 144 BY SIMILARITY.
CC SQ SEQUENCE 365 AA; 40713 MW; 2c8779BD648925A4 CRC64;

Query Match 61.6%; Score 45; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. No. 0.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIHS 15
DB 36 IDRLVSIRTRGOIHS 50

RESULT 6
AMYLORISA STANDARD: PRT; 428 AA.
AC P17654;
DR 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Isozyme 1b).
GN AMY1.1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Japonica M202;
RX MEDLINE-91346657; PubMed-2102847;
RA Huang N., Sutliff T.D., Lits J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amylase
RT multigene family."
RT Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POST03).
RC STRAIN-CV. Japonica M202;
RX MEDLINE-90318322; PubMed-2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;

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RT "The alpha-amylase genes in Oryza sativa: Characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Gen. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALLUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PTM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16509; CAA34516.1; -
CC EMBL: M24286; AAA33885.1; ALT_INIT.
CC DR PIR; S10013; S10013.
CC DR HSSP; P04063; IAVA.
CC DR Gramene: P17654; -
CC DR InterPro: IPR006589; Alp_amy1_cat_sub.
CC DR InterPro: IPR006047; Alpha_amy1_cat.
CC DR InterPro: IPR006046; Glyco_hydro_13.
CC DR Pfam: PF00128; alpha-amylase; 1.
CC DR PRINTS: PR00110; ALPHAMYLASE.
CC DR SMART; SM00642; Amy; 1.
CC KM Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
CC KM Glycoprotein; Multigene family.
CC FT SIGNAL 1 25 PROBABLE.
CC FT CHAIN 26 428 ALPHA-AMYLASE.
CC FT ACT_SITE 203 203 BY SIMILARITY.
CC FT ACT_SITE 314 314 BY SIMILARITY.
CC FT METAL 116 116 CALCIUM (BY SIMILARITY).
CC FT METAL 174 174 CALCIUM (BY SIMILARITY).
CC FT CARBOHYD 265 265 N-LINKED (GLCNAC...) (PROBABLE).
CC SQ SEQUENCE 428 AA; 47755 MW; 3B71403AACF6C6A6 CRC64;

Query Match 61.6%; Score 45; DB 1; Length 428;
Best Local Similarity 71.4%; Pred. No. 0.6;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
DB 359 IDRLVSIRTRGOIH 372

RESULT 7
AMY3_HORVU STANDARD: PRT; 368 AA.
AC P04747;
DR 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUN-1999 (Rel. 38, Last annotation update)
DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase) (Clone PHV19) (Fragment).
GN AMY3.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]

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RP SEQUENCE FROM N.A.
RA Chander P.M., Zwar J.A., Jacobsen J.V., Higgins T.J.V., Inglis A.S.;
RT "The effects of gibberellic acid and abscisic acid on alpha-amylase
RT mRNA levels in barley aleurone layers studies using an alpha amylase
RT cDNA clone.";
RL Plant Mol. Biol. 3:407-418(1984).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS NORMALLY
CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC
CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
CC THEN DEGRADS THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
CC DEVELOPING PLANT EMBRYO.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
CC GIBBERELIC ACID.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL; K02638; AAA32933.1; -.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR SMART; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family; Signal.
FT SIGNAL 1 24
FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 228 228 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;

Query Match 54.8%; Score 40; DB 1; Length 368;
Best Local Similarity 88.9%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDRLVSIRT 9
DB 358 IDRLVSIRT 366

RESULT 8
NRH3_MOUSE STANDARD; PRT; 445 AA.
AC Q9Z0Y9; Q9Z0Y7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxyterol receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
DE receptor LXR-alpha).
GN NR1H3 OR LXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCI_TaxID=10090;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;

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RX MEDLINE=20156373; PubMed=10675617;
RA Alberti S., Steffensen K.R., Gustafsson J.-A.;
RT "Structural characterisation of the mouse nuclear oxysterol receptor
RT gene LXRalpha and LXRbeta.";
RL Gene 243:93-103(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen Y.E., Horiuchi M., Dzau V.J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
CC ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
CC BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
CC GENES. DEFINED BY LXRES. LXRES ARE DR-1-TYPE RESPONSE ELEMENTS
CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
CC SITES SPACED BY FOUR NUCLEOTIDES. LXRA PLAYS AN IMPORTANT ROLE IN
CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS.
CC -1- SUBUNIT: HETERODIMER OF LXRA AND RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
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CC -----
DR EMBL; AJ132599; CAB51952.1; -.
DR EMBL; AJ132600; CAB51952.1; JOINED.
DR EMBL; AJ132601; CAB51923.1; -.
DR EMBL; AF085745; AAD16050.1; -.
DR HSSP; P03372; IHCO.
DR TRANSFAC; T04430; -.
DR MGD; MGI:1352462; Nr1h3.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroidm_receptor.
DR InterPro; IPR001628; Znfc4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR PRINTS; PR00105; zf-C4; 1.
DR PRINTS; PR00398; STROHOMONER.
DR PRINTS; PR00047; STRODFINGER.
DR PRODOM; PD000035; Znfc4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znfc4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 96 161 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 96 116 C4-TYPE.
FT ZN_FING 132 156 C4-TYPE.
FT DOMAIN 213 432 LIGAND-BINDING (POTENTIAL).
FT CONFLICT 399 399 R -> P (IN REF. 2).
SQ SEQUENCE 445 AA; 50476 MW; CC9A8DF38D935593 CRC64;

Query Match 53.4%; Score 39; DB 1; Length 445;
Best Local Similarity 53.8%; Pred. No. 9.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIKRGDIHS 15
DB 408 KLVSLRPLSSVHS 420

RESULT 9
NRH3_RAT STANDARD; PRT; 445 AA.
AC Q62685;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxyterol receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
DE receptor LXR-alpha).
GN NR1H3 OR LXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCI_TaxID=10090;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Liver;

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DE receptor LXR-alpha) (RLD-1).
GN NRH3 OR LXRA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RA MEDLINE=95021230; PubMed=7935418;
RA Apfel R.H., Bendbrook D., Lernmark E., Ottiz M.A., Salbert G.,
RA Pfahl M.;
RT "A novel orphan receptor specific for a subset of thyroid hormone-
RT responsive elements and its interaction with the retinoid/thyroid
RT hormone receptor subfamily."
RL Mol. Cell. Biol. 14:7025-7035(1994).
CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
CC ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
CC BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
CC GENES DEFINED BY LXRES. LXRES ARE DR4-TYPE RESPONSE ELEMENTS
CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
CC SITES SPACED BY FOUR NUCLEOTIDES. LXRA PLAYS AN IMPORTANT ROLE IN
CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF LXRA AND RXR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: IN ADULTS IT IS EXPRESSED IN SPLEEN,
CC PITUITARY, LUNG, LIVER, AND FAT. WEAKER EXPRESSION IS OBSERVED IN
CC SEVERAL OTHER TISSUES.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U01685; AA053633.1;
DR PIR: A36043; A56043.
DR HSSP: P03372; IHCO.
DR TRANSFAC: T04434.
DR InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001723; Sterhmr_receptor.
DR InterPro: IPR001628; ZnF_C4steroid.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STROHOMNER.
DR PRINTS: PR00047; STROIDFNGER.
DR ProDom: PD000035; ZnF_C4steroid; 1.
DR SMART: SM00430; HOL1; 1.
DR SMART: SM00399; ZnF_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor: Transcription regulation; DNA-binding; Nuclear protein;
DR Zinc-finger.
KW DNA_BIND.
FT ZN_FING. 96 116 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING. 132 156 C4-TYPE.
FT DOMAIN 213 432 LIGAND-BINDING (POTENTIAL).
SQ SEQUENCE 445 AA; 50554 MW; 111A84AB1A2A82 CRC64;

Query Match 53.4%; Score 39; DB 1; Length 445;
Best Local Similarity 53.8%; Pred. No. 9.1;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

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ID NRH2 MOUSE STANDARD; PRT; 446 AA.
AC 060644.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxyesterols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan
DE Oxyesterols receptor LXR-beta) (ubiquitously-expressed nuclear receptor) (Retinoid
DE X receptor interacting protein No.15).
GN NRH2 OR LXRB OR UNR2 OR UNR OR RIP15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=95280959; PubMed=7760852;
RA Seol W., Choi H.S., Moore D.D.;
RT "Isolation of proteins that interact specifically with the retinoid X
RT receptor: two novel orphan receptors."
RL Mol. Endocrinol. 9:72-85(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Svj; TISSUE=Liver;
RX MEDLINE=20156373; PubMed=10675617;
RA Alberti S., Steffensen K.R., Gustafsson J.-A.;
RT "Structural characterisation of the mouse nuclear oxyesterol receptor
RT genes LXRAalpha and LXRBeta."
RL Gene 243:93-103(2000)
CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
CC SEQUENCE 5'-AGGCA-3' AND A-NT SPACING (DR-4).
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U09419; AAC52164.1;
DR PIR: A132602; CAB51924.1;
DR HSSP: P03372; IHCO.
DR TRANSFAC: T04467;
DR MGD: MGI:1352463; Nr1h2.
DR InterPro: IPR000536; Hormone_rec_1lg.
DR InterPro: IPR001723; Sterhmr_receptor.
DR InterPro: IPR001628; ZnF_C4steroid.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STROHOMNER.
DR PRINTS: PR00047; STROIDFNGER.
DR ProDom: PD000035; ZnF_C4steroid; 1.
DR SMART: SM00430; HOL1; 1.
DR SMART: SM00399; ZnF_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR Receptor: Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND. 78 145 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING. 78 98 C4-TYPE.
FT ZN_FING. 116 140 C4-TYPE.
FT DOMAIN 216 446 LIGAND-BINDING (POTENTIAL).
FT DOMAIN 162 168 POLY-GLN.
FT DOMAIN 169 172 POLY-PRO.
SQ SEQUENCE 446 AA; 49719 MW; 73153E635302C9DF CRC64;

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RESULT 10
NRH2_MOUSE

Query Match 53.4%; Score 39; DB 1; Length 446;
 Best Local Similarity 53.8%; Pred. No. 9.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

3 RLVSIPTRGQIHS 15
 :|||:|:|:|
 Db 409 KLVSLRTLSVHS 421

RESULT 11
 ID NRH2_RAT STANDARD; PRT; 446 AA.
 AC 062755: 062694;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oxytelols receptor LXR-beta (Liver X receptor beta) (Nuclear orphan
 receptor LXR-beta) (Ubiquitously-expressed nuclear receptor) (UR
 (Orphan nuclear receptor OR-1)).
 GN NRH2 OR LXRβ.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95199298; PubMed=7892230;
 RA Teboul M., Emek E., Li Q., Wikstrom A.C., Pelto-Huikko M.,
 RA Gustafsson J.-A.;
 RT "OR-1, a member of the nuclear receptor superfamily that interacts
 with the 9-cis-retinoic acid receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2096-2100(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Vagina;
 RX MEDLINE=95062154; PubMed=7971966;
 RA Song C., Kokontis J.M., Hlipakka R.A., Liao S.;
 RT "Ubiquitous receptor: a receptor that modulates gene activation by
 retinoic acid and thyroid hormone receptors."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10809-10813(1994).
 CC -1- ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
 OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
 SEQUENCE 5'-AGGTCA-3' AND 4'-NT SPACING (DR-4).
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
 subfamily.
 CC -----
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 CC -----
 CC EMBL: U20389; AAA69522.1; -;
 DR EMBL: U14533; AAA52361.1; -;
 DR PIR: I59354; I59354.
 DR HSSP: P03372; IHCO.
 DR TRASNAC: T04451; -;
 DR InterPro: IPR000536; Hormone_rec_119.
 DR InterPro: IPR001723; Stchmn_receptor.
 DR InterPro: IPR001628; znf_C4steroid.
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; znf_C4.1.
 DR PRINTS: PR00396; STRDHOMONER.
 DR PRINTS: PR00047; STROIDFINGER.
 DR PRODOM: PD000035; znf_C4steroid.1.
 DR SMART: SM00430; HOLT.1.
 DR SMART: SM00399; znf_C4.1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR.1.

KW Receptor: Transcription regulation: DNA-binding; Nuclear protein;
 KW Zinc-finger. 78 145
 FT ZN_FING 78 98
 FT ZN_FING 116 140
 FT DOMAIN 216 446
 FT DOMAIN 162 168
 FT DOMAIN 169 172
 FT CONFLICT 33 33
 FT CONFLICT 52 54
 FT CONFLICT 219 219
 SQ SEQUENCE 446 AA; 49735 MW; 13DF6DC2F0F5FA4D CRC64;

Query Match 53.4%; Score 39; DB 1; Length 446;
 Best Local Similarity 53.8%; Pred. No. 9.1;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

3 RLVSIPTRGQIHS 15
 :|||:|:|:|
 Db 409 KLVSLRTLSVHS 421

RESULT 12
 ID NRH3_HUMAN STANDARD; PRT; 447 AA.
 AC Q13133; 096h87;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Oxytelols receptor LXR-alpha (Liver X receptor alpha) (Nuclear orphan
 receptor LXR-alpha).
 GN NRH3 OR LXRα.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=95262897; PubMed=7744246;
 RA Willy P.J., Umesono K., Ong E.S., Evans R.M., Heyman R.A.,
 RA Mangelsdorf D.J.;
 RT "LXR, a nuclear receptor that defines a distinct retinoid response
 pathway."
 RL Genes Dev. 9:1033-1045(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin J., Hong L.,
 RA Staphenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION WITH RXR SHIFTS RXR FROM
 ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-
 BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET
 GENES DEFINED BY LXRS. LXRS ARE DR4-TYPE RESPONSE ELEMENTS

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CC CHARACTERIZED BY DIRECT REPEATS OF TWO SIMILAR HEXANUCLEOTIDE HALF-
CC SITES SPACED BY FOUR NUCLEOTIDES. LXRA PLAYS AN IMPORTANT ROLE IN
CC THE REGULATION OF CHOLESTEROL HOMEOSTASIS.
CC -1- SUBUNIT: HETERODIMER OF LXRA AND RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q13133-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q13133-2; Sequence=VSP_003664;
CC Note=No experimental confirmation available.
CC -1- TISSUE SPECIFICITY: VISCERAL ORGANS SPECIFIC EXPRESSION. STRONG
CC EXPRESSION WAS FOUND IN LIVER, KIDNEY AND INTESTINE FOLLOWED BY
CC SPLEEN AND TO A LESSER EXTENT THE ADRENALS.
CC -1- INDUCTION: BY 9-CIS RETINOIC ACID (9CRA).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
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CC -----
CC EMBL: U22662; AAA85856.1; -.
CC DR EMBL: BC008819; AAH08819.1; -.
CC DR PIR: I38975; I38975.
CC DR HSSP: P03372; IHCO.
CC DR TRANSFAC: T02752; -.
CC DR Genew: HGNC:7966; NR1H3.
CC DR MIM: 602423; -.
CC DR GO: GO:0005634; C:nucleus; TAS.
CC DR GO: GO:0003713; F:transcription co-activator activity; TAS.
CC DR InterPro: IPR000536; Hormone_rec_lig.
CC DR InterPro: IPR001723; Stbhm_receptor.
CC DR InterPro: IPR001628; znf_Csteroid.
CC DR Pfam: PF00104; hormone_rec; 1.
CC DR Pfam: PF00105; zfc-C4; 1.
CC DR PRINTS: PR00398; STROPHOMONER.
CC DR PRODOM: PD000035; znf_C4steroid; 1.
CC DR SMART: SM00330; HOL1; 1.
CC DR SMART: SM00330; znf_C4; 1.
CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
CC DR PROSITE: PS00031; NUCLEAR_RECEPTOR; DNA-binding; Nuclear protein;
CC KW Zinc-finger; Alternative splicing.
CC FT DNAS_BIND 98 163 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 98 118 C4-TYPE.
CC FT ZN_FING 134 158 C4-TYPE.
CC FT DOMAIN 215 434 LIGAND-BINDING (POTENTIAL).
CC FT VARSPLIC 237 296 Missing (in isoform 2).
CC FT CONFLICT 196 196 A -> R (in REF. 1).
CC SQ SEQUENCE 447 AA; 50395 MW; 0D27B37440F89C CRC64;
CC Query Match 53.4%; Score 39; DB 1; Length 447;
CC Best Local Similarity 53.8%; Pred. No. 9.1;
CC Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Oxytocin receptor LXR-beta (Liver X receptor beta) (Nuclear orphan
DE receptor LXR-beta) (ubiquitously-expressed nuclear receptor) (Nuclear
DE receptor NER)
GN NR1H2 OR LXRβ OR UNR OR NER.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleia; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Osteosarcoma;
RX MEDLINE=95011628; PubMed=7926814;
RA Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
RT "NER, a new member of the gene family encoding the human steroid
RT hormone nuclear receptor."
RT gene 147:273-276(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Diatchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Merra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 7-461 FROM N.A.
RA Song C., Konkolis J.M., Hilpakka R.A., Liao S.,
RT "Ubiquitous receptor: a novel receptor that modulates gene activation
RT by retinoic acid and thyroid hormone receptors."
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
CC OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
CC SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
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CC -----
CC EMBL: U07132; AAA61783.1; -.
CC DR EMBL: BC007790; AAH07790.1; -.
CC DR EMBL: U14534; AAA58594.1; -.
CC DR PIR: JC4014; JC4014.
CC DR HSSP: P03372; IHCO.
CC DR TRANSFAC: T04453; -.
CC DR Genew: HGNC:7965; NR1H2.
CC DR MIM: 600380; -.
CC DR GO: GO:0005634; C:nucleus; TAS.

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DR InterPro: IPR000536; Hormone_rec.1lg.
 DR InterPro: IPR001723; Stdhmm_receptor.
 DR InterPro: IPR001628; Znf_C4steroid.
 DR Pfam: PF00104; hormone_rec.1.
 DR Pfam: PF00105; zf-C4.1.
 DR PRINTS: PRO0398; STRDHOMONER.
 DR PROSITE: PS00047; STROIDFINGER.
 DR PRODOM: PD000035; Znf_C4steroid.1.
 DR SMART: SM00430; HOL1.1.
 DR SMART: SM00399; Znf_C4.1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR.1.
 KW Receptor: Transcription regulation; DNA-binding; Nuclear protein;
 ZINC-finger.
 FT DNABIND 87 154 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 87 107 C4-TYPE.
 FT ZN_FING 125 149 C4-TYPE.
 FT DOMAIN 231 461 LIGAND-BINDING (POTENTIAL).
 FT DOMAIN 173 176 POLY-GLN.
 FT DOMAIN 191 196 POLY-SER.
 SQ SEQUENCE 461 AA; 5102 MW; 68CE3D9F9BC5C0BE CRC64;

Query Match 53.4%; Score 39; DB 1; Length 461;
 Best Local Similarity 53.8%; Pred. No. 9.4;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 3 RLVSIRTRGQIHS 15
 :||:|:|:|:|
 DB 424 KLVSIRTRLSVSHS 436

RESULT 14
 YB13_YEAST STANDARD; PRT; 585 AA.
 AC P38289;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Hypothetical 67.6 kDa protein in CDC28-ARL1 Intergenic region.
 GN YBR163W OR YBR1215.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RA Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
 RA Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
 RA Wolter R., Brendel M., Bauer J., Braun H., Derr K., Duesterhus S.,
 RA Gruenbein R., Hedges D., Kriesau P., Korol S., Krebs B., Prott M.,
 RA Slegers K., Baur A., Boles E., Miosga T.,
 RA Schait-Gerstenschlaeger I., Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL: Z36032; CAA85123.1; -.
 DR PIR: S46034; S46034.
 DR SCD: S0000367; DEM1.
 KW Hypothetical protein.
 SQ SEQUENCE 585 AA; 67569 MW; 92DBE35B819F0A9B CRC64;

Query Match 53.4%; Score 39; DB 1; Length 585;
 Best Local Similarity 53.3%; Pred. No. 12;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 1 IDRLVSIRTRGQIHS 15

DB 218 INRLVSLFTKGDGHA 232

RESULT 15
 RRP5_YEAST STANDARD; PRT; 1729 AA.
 ID RRP5_YEAST
 AC Q05022;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE RNA biogenesis protein RRP5.
 GN RRP5 OR FMI1 OR YMR229C OR YMG959.11C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RC PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
 RA Jagers K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT XIII."
 RL Nature 387:90-93(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=97051828; PubMed=8896463;
 RA Venema J., Tollervey D.;
 RT "RRP5 is required for formation of both 18S and 5.8S rRNA in yeast."
 RL EMBO J. 15:5701-5714(1996).
 CC -1- FUNCTION: INVOLVED IN THE BIOGENESIS OF RRNA. REQUIRED FOR THE
 CC FORMATION OF 18S AND 5.8S RRNA.
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -1- SIMILARITY: Contains 4 HAT repeats.
 CC -1- SIMILARITY: Contains 11 S1 motif domains.
 CC -----
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 CC -----
 CC EMBL: Z49939; CAA90200.1; -.
 DR PIR: S57596; S57596.
 DR HSSP: P05055; ISRO.
 DR SCD: S0004842; RRP5.
 DR GO: GO:0005731; C:nucleolus organizer complex; IPI.
 DR GO: GO:0030515; F:snRNA binding activity; IPI.
 DR GO: GO:0030490; P:processing of 20S pre-rRNA; IPI.
 DR InterPro: IPR003107; HAT.
 DR InterPro: IPR003029; S1.
 DR Pfam: PF00575; S1.7.
 DR SMART: SM00386; HAT; 6.
 DR SMART: SM00316; S1; 12.
 DR PROSITE: PS50126; S1; 11.
 KW Nuclear protein; rRNA processing; Repeat.
 FT DOMAIN 119 200 S1 MOTIF 1.
 FT DOMAIN 338 410 S1 MOTIF 2.
 FT DOMAIN 510 580 S1 MOTIF 3.
 FT DOMAIN 607 676 S1 MOTIF 4.
 FT DOMAIN 690 769 S1 MOTIF 5.
 FT DOMAIN 794 863 S1 MOTIF 6.
 FT DOMAIN 895 971 S1 MOTIF 7.
 FT DOMAIN 1003 1083 S1 MOTIF 8.
 FT DOMAIN 1088 1159 S1 MOTIF 9.
 FT DOMAIN 1177 1245 S1 MOTIF 10.
 FT DOMAIN 1265 1336 S1 MOTIF 11.

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FT REPEAT 1455 1487 HAT 1.
FT REPEAT 1561 1594 HAT 2.
FT REPEAT 1632 1664 HAT 3.
FT REPEAT 1666 1701 HAT 4.
SQ SEQUENCE 1729 AA; 193133 MW; 39BF46E5587B3B0A CRC64;

Query Match 53.4%; Score 39; DB 1; Length 1729;
Best Local Similarity 41.7%; Pred. No. 42;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RUVSIRTRGOIH 14
DB 565 RUVSIRTRGOIH 576

RESULT 16
YH01_YEAST STANDARD; PRT; 223 AA.
AC P38736;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Hypothetical 25.4 kDa protein in GUT1-RIM1 intergenic region.
GN YH031C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dwyer J.,
RA Du Z., Favell A., Fulton L., Gattung S., Gelsel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mandis E., Menezes S., Mouser L.,
RA Phan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vandin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -!- SIMILARITY: TO S.FOMBE SPAC48.10.
CC -----
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CC -----
DR EMBL: U11583; AAB65043.1; -.
DR PIR: S48937; S48937.
DR SGD: S0001023; GOSL.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR Pfam: PF05008; V-SNARE; 1.
KM Hypothetical protein.
SQ SEQUENCE 223 AA; 25394 MW; 1E833249CC306C2 CRC64;

Query Match 52.1%; Score 38; DB 1; Length 223;
Best Local Similarity 52.9%; Pred. No. 6;
Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 IDRLVSIIRTRGOIH 15
DB 152 VDRLSQAMETRSQFHS 168

RESULT 17
YH01_YEAST STANDARD; PRT; 319 AA.
AC Q00122;

```

```

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hypothetical gene 61 protein.
GN 61
OS Ictalurid herpesvirus 1 (channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid Herpes-like viruses.
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Addison 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC -----
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CC -----
DR EMBL: M75136; AAA88164.1; -.
DR PIR: H36792; H36792.
KM Hypothetical protein.
SQ SEQUENCE 319 AA; 36909 MW; 253E93AE41815143 CRC64;

Query Match 52.1%; Score 38; DB 1; Length 319;
Best Local Similarity 46.2%; Pred. No. 9;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDRLVSIIRTRGOI 13
DB 213 VDRLGRKLRARREV 225

RESULT 18
YH02_YEAST STANDARD; PRT; 365 AA.
AC P28625;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 41.6 kDa protein in IMPI-HLJ1 intergenic region (RF1095).
GN YMR152W OR YM9375.22 OR YM8520.01.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=91360060; PubMed=1886606;
RA Behrens M., Michaelis G., Prate E.;
RT "Mitochondrial inner membrane protease 1 of Saccharomyces cerevisiae
RT shows sequence similarity to the Escherichia coli leader peptidase.";
RL Mol. Gen. Genet. 228:167-176(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jags R., Kellon J., Lye G., Moutie S., Odell C., Pearson D., Rajadream M.A.,
RA Rice R., Skelton J., Walsh S., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XII."
RL Nature 387:90-93(1997).
CC -!- SIMILARITY: SOME, TO YEAST AST1/AST2.
CC -----
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 DR EMBL: S55518; AAB19702.1; -
 DR EMBL: Z47071; CAA87367.1; -
 DR EMBL: Z49705; CAA89788.1; -
 DR PIR: S50409; S50409.
 DR SGD: S0004760; YIM1.
 DR GO: GO:0005811; C:lipid particle; IDA.
 DR GO: GO:0005743; C:mitochondrial inner membrane; IDA.
 DR GO: GO:0008233; F:peptidase activity; IMP.
 DR GO: GO:0006627; P:mitochondrial processing; IMP.
 DR InterPro: IPR002085; Adh_zn_family.
 DR Pfam: PF00107; ADH_zinc_N; 1.
 DR Hypothetical protein; Transmembrane.
 KW TRANSMEM 140 158 POTENTIAL.
 FT CONFLICT 121 121 V -> I (IN REF. 1).
 FT CONFLICT 234 234 S -> I (IN REF. 1).
 FT CONFLICT 280 280 D -> N (IN REF. 1).
 FT CONFLICT 296 296 L -> S (IN REF. 1).
 SQ SEQUENCE 365 AA; 41637 MW; 88F6453D9E918A16 CRC64;

 Query Match 52.1%; Score 38; DB 1; Length 365;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

 QY 1 IDRLVSIRTRGOI 13
 Db 348 IDRLMSNRKGV 360

 RESULT 19
 RL17_THETH STANDARD: PRT; 118 AA.
 AC Q929H5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ OR RPL17.
 OS Thermus thermophilus.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=274;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RA MEDLINE=99098837; PubMed=9880810;
 RA Wada T., Yamazaki T., Kuramitsu S., Kyogoku Y.;
 RT "Cloning of the RNA polymerase alpha subunit gene from Thermus
 thermophilus HB8 and characterization of the protein.";
 RL J. Biochem. 125:143-150(1999).
 CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.

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 DR EMBL: AB024328; BAA75550.1; -
 DR PDB: 1GD8; 28-JAN-03.
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR ProDom: PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; FALSE_NEG.

KW Ribosomal protein; 3D-structure.
 SQ SEQUENCE 118 AA; 13715 MW; C9B8D552F6C42AF CRC64;

 Query Match 50.7%; Score 37; DB 1; Length 118;
 Best Local Similarity 33.3%; Pred. No. 5;
 Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

 QY 1 IDRLVSIRTRGOIHS 15
 Db 48 VDHLIRLAKRGDLHA 62

 RESULT 20
 RL17_MYCA STANDARD: PRT; 119 AA.
 ID IDL17_MYCA
 AC Q48980;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein (Fragment).
 GN RPLQ.
 OS Mycoplasma capricolum.
 OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
 OC Entomoplasmataceae.
 OX NCBI_TaxID=2095;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27343 / Kid;
 RX MEDLINE=96059641; PubMed=7476192;
 RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M.,
 RA Gilbert W., Gillet P.M.;
 RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
 RT its physiology.";
 RL Mol. Microbiol. 16:955-967(1995).
 CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.

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 DR EMBL: Z33050; CAA83721.1; -
 DR PIR: S77863; S77863.
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR ProDom: PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; FALSE_NEG.
 KW Ribosomal protein.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 13896 MW; 420CEADA708A9FEB CRC64;

 Query Match 50.7%; Score 37; DB 1; Length 119;
 Best Local Similarity 35.7%; Pred. No. 5;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

 QY 2 DRLVSIRTRGOIHS 15
 Db 46 DHMITLAKRGDLHS 59

 RESULT 21
 RL17_RHIME STANDARD: PRT; 141 AA.
 ID IDL17_RHIME
 AC Q926A5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ OR R01381 OR SMC01283.


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OC Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RA Peck M.C., Fisher R.F., Long S.R.;
RT "Isolation and characterization of RpoA from Rhizobium meliloti.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaune V., Maury D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ransperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc Natl Acad Sci U S A. 98:9877-9882(2001).
CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
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-----
CC EMBL: AF317474; AL26902.1; -
CC EMBL: AL591787; CAC45960.1; -
CC DR InterPro: IPR000456; Ribosomal_L17.
CC DR Pfam: PF01196; Ribosomal_L17.1.
CC DR ProDom: PD004277; Ribosomal_L17.1.
CC DR TIGRFAMs: TIGR00059; L17.1.
CC DR PROSITE: PS01167; RIBOSOMAL_L17.1.
CC DR Ribosomal protein; Complete proteome.
CC KW SEQUENCE 141 AA; 15492 MW; 351EB47A113C14D8 CRC64;
SO
Query Match 50.7%; Score 37; DB 1; Length 141;
Best Local Similarity 33.3%; Pred. No. 6.1;
Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
OY 1 IDRLVSRTRGQIHS 15
DB 48 VEKLVTLGKRGLDHA 62
-----
RESULT 22
VNS3_CVCAI STANDARD; PRT; 250 AA.
ID VNS3_CVCAI
AC P36693;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nonstructural protein 3-B (ORF 3B).
OS Canine enteric coronavirus (strain Insavc-1) (CCOV) (CCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=36391;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93057357; PubMed=1431811;
RA Horsburgh B.C., Brierley I., Brown T.D.K.;
RT "Analysis of a 9.6 kb sequence from the 3' end of canine coronavirus
RT genomic RNA.";
RL J. Gen. Virol. 73:2849-2862(1992).
CC -1- SIMILARITY: Belongs to the coronavirus NS3b protein family.
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-----
CC EMBL: D13096; BAA02411.1; ALT_TERM.
CC DR InterPro: IPR004293; Corona_NS3b.
CC DR Pfam: PF03053; Corona_NS3b.1.
CC Nonstructural protein.
CC KW SEQUENCE 250 AA; 28426 MW; FCB7ABFD83DD9CPE CRC64;
SO
Query Match 50.7%; Score 37; DB 1; Length 250;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 4 LVSPTRRGQIHS 15
DB 178 LVSTATRGIAHA 189
-----
RESULT 23
TRC2_STRCO STANDARD; PRT; 258 AA.
ID TRC2_STRCO
AC Q924X0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Indole-3-glycerol phosphate synthase 2 (EC 4.1.1.48) (IGPS 2).
GN TRP2 OR SCO3211 OR SCEB_04C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Streptomyces; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Horsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- FUNCTION: THE FUNCTION OF THE SECOND TRP OPERON IN S.COELICOLOR IS
CC TO PRODUCE TRP FOR THE BIOSYNTHESIS OF CALCIUM-DEPENDENT
CC ANTI-BIOTIC (CDA).
CC -1- CATALYTIC ACTIVITY: 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-
CC phosphate - 1-(indol-3-yl)glycerol 3-phosphate + CO(2) + H(2)O.
CC -1- PATHWAY: Tryptophan biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE TRP2 FAMILY.
-----
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-----
CC EMBL: AL035654; CAB38582.1; -
CC DR PIR: T36303; T36303.
CC DR HSSP: P00909; IPTI.
CC DR HAMAP: MF_00134; -.1.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001468; IGPS.

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DR Pfam; PF00218; IGPS; 1.
 DR PRODOM; PD001511; IGPS; 1.
 DR PROSITE; PS00614; IGPS; 1.
 KW Tryptophan biosynthesis; Lyase; Decarboxylase;
 KM Antibiotic biosynthesis; Complete proteome.
 SO SEQUENCE 258 AA; 26815 MW; BZA3JBFA85C642A CRC64;

Query Match 50.7%; Score 37; DB 1; Length 258;
 Best Local Similarity 53.8%; Pred. No. 12;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOI 13
 DB 196 IDRLTSLAKLRGRV 208

RESULT 24
 T4HR_MAGGR STANDARD; PRT; 282 AA.
 AC Q12634;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tetrahydroxynaphthalene reductase (EC 1.1.1.252) (T4HN reductase)
 DE (TMNR).
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=Guyane 11;
 RA MEDLINE=94155906; PubMed=8112349;
 RA Vidal-Cros A., Viviani F., Labesse G., Boccard M., Gaudy M.;
 RT "Polyhydroxynaphthalene reductase involved in melanin biosynthesis in
 RT Magnaporthe grisea. Purification, cDNA cloning and sequencing.";
 RL Eur. J. Biochem. 219:985-992(1994).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RC STRAIN=4091-5-8;
 RA MEDLINE=97094973; PubMed=8939741;
 RA Andersson A., Jordan D., Schneider G., Lindqvist Y.;
 RT "Crystal structure of the ternary complex of
 RT 1,3,8-trihydroxynaphthalene reductase from Magnaporthe grisea with
 RT NADPH and an active-site inhibitor";
 RL Structure 4:1161-1170(1996).
 CC -1- FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF 1,3,6,8-
 CC TETRAHYDROXYNAPHTHALENE (T4HN) INTO (+)-SCYTALONE AND 1,3,8-
 CC TRIHYDROXYNAPHTHALENE INTO (-)-VERMELONE. THIS ENZYME IS THE
 CC BIOCHEMICAL TARGET OF SEVERAL COMMERCIALY IMPORTANT FUNGICIDES
 CC WHICH ARE USED TO PREVENT BLAST DISEASE IN RICE PLANTS.
 CC -1- CATALYTIC ACTIVITY: Scytalone + NADP(+) = 1,3,6,8-
 CC tetrahydroxynaphthalene + NADPH.
 CC -1- PATHWAY: Fungal melanin biosynthesis.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL; L22309; AA19514.1; -;
 DR PIR; S41412; S41412.
 DR PDB; 1YBV; 15-OCT-97.
 DR PDB; IDOH; 06-JUN-01.
 DR PDB; 1G0N; 06-JUN-01.
 DR PDB; 1G0O; 06-JUN-01.
 DR InterPro; IPR002198; ADH_short.

DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase; NADP; Melanin biosynthesis; 3D-structure.
 FT INIT_MER 0 0
 FT NP_BIND 32 56 NADP (BY SIMILARITY).
 FT ACT_SITE 177 177
 FT HELIX 21 24
 FT TURN 27 28
 FT STRAND 29 33
 FT TURN 34 35
 FT HELIX 39 50
 FT TURN 51 52
 FT STRAND 53 59
 FT HELIX 63 75
 FT TURN 76 77
 FT STRAND 80 84
 FT TURN 87 88
 FT HELIX 90 104
 FT STRAND 109 112
 FT HELIX 122 124
 FT TURN 127 137
 FT HELIX 138 138
 FT TURN 139 151
 FT STRAND 154 155
 FT TURN 157 161
 FT HELIX 164 166
 FT TURN 167 167
 FT HELIX 175 194
 FT TURN 195 198
 FT TURN 199 199
 FT STRAND 201 207
 FT TURN 210 210
 FT HELIX 213 218
 FT TURN 219 221
 FT HELIX 222 222
 FT TURN 224 225
 FT TURN 227 228
 FT HELIX 231 241
 FT TURN 244 245
 FT STRAND 249 249
 FT HELIX 251 262
 FT TURN 264 268
 FT STRAND 272 276
 SO SEQUENCE 282 AA; 29922 MW; 2520709137763087 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 282;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DRLVSIIRTRGO 12
 DB 131 DRVFTIRTRGO 141

RESULT 25
 ISPE_CORGL STANDARD; PRT; 311 AA.
 AC Q8NRV0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 4-diphosphocytidyl-2-C-methyl-D-erythritol Kinase (EC 2.7.1.148) (CMK)
 DE (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).
 GN ISPE OR CGL0911.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;

RT "Complete genomic sequence of *Corynebacterium glutamicum* ATCC 13032.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
CC group of 4-diphosphocytidylyl-2C-methyl-D-erythritol (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
CC erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
CC methyl-D-erythritol.
CC -1- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
CC step.
CC -1- SIMILARITY: BELONGS TO THE ISPE FAMILY.
CC -----
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CC -----
CC EMBL: AP005276; BAB98304.1; -.
DR HAMAP: MF_00061; -; 1.
DR InterPro: IPR006204; GHMP_Kinase.
DR InterPro: IPR004424; ISPE.
DR Pfam: PF00288; GHMP_Kinases; 1.
DR TIGRFAMs: TIGR00154; ispe; 1.
DR Transferase: Kinase; Isoprene biosynthesis; ATP-binding;
KM Complete proteome.
FT NP_BIND 105 115 ATP (POTENTIAL).
SQ SEQUENCE 311 AA; 32630 MW; 392FD92100D040F8 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 311;
Best Local Similarity 46.2%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 DRVSIRTRGOIH 14
Db 163 EQALVDMLTRGKLH 175

RESULT 26
F16P-SHEEP STANDARD; PRT; 336 AA.
ID F16P-SHEEP
AC P09199;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
DE 1-phosphohydrolyase) (FBPase).
GN FBP1 OR FBP.
OS Ovis aries (Sheep).
OC Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=84079343; PubMed=6316885;
RA Fisher W.K., Thompson E.O.P.;
RT "Amino acid sequence studies on sheep liver fructose-bisphosphatase.
RT II. The complete sequence.";
RL Aust. J. Biol. Sci. 36:235-250(1983).
RN [2]
RP SEQUENCE OF 1-60.
RX MEDLINE=81232062; PubMed=6264908;
RA Fisher W.K., Thompson E.O.P.;
RT "Amino acid sequence studies on sheep liver fructose-bisphosphatase.
RT I. The S-peptide.";
RL Aust. J. Biol. Sci. 33:655-674(1980).
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H2O = D-
CC fructose 6-phosphate + phosphate.
CC -1- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER
CC OF BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.

CC -1- PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMOTETRAMER, WITH FOUR BINDING SITES
CC EACH FOR THE SUBSTRATE FOR AMP, AND FOR DIVALENT METAL CATION
CC (THE GREATEST AFFINITY IS FOR ZINC).
CC -1- SIMILARITY: BELONGS TO THE FBPA FAMILY.
DR PIR: A05318; A05318.
DR HSSP: P00636; ATP.
DR InterPro: IPR00146; IN_FB_phphatase.
DR Pfam: PF00310; FBPAse; 1.
DR PRINTS: PR001491; IN_FB_phphatase.
DR PRODOM: PD001491; IN_FB_phphatase; 1.
DR PROSITE: PS00124; FBPAse; 1.
KM Hydrolyase; carbonylate metabolism; Gluconeogenesis; Acetylation;
KM Phosphorylation; Zinc Allosteric enzyme.
FT INT_MET 0 1 ACETYLATION.
FT MOD_RES 141 141 ALLOSTERIC REGULATION BY AMP.
FT BINDING 207 207 PHOSPHORYLATION (BY PKA).
FT MOD_RES 274 274 BY SIMILARITY.
FT ACT_SITE 356 356 BY SIMILARITY.
SQ SEQUENCE 336 AA; 36544 MW; 2E9826BA50EC925E CRC64;

Query Match 50.7%; Score 37; DB 1; Length 336;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDRVISIRTRGOIHS 15
Db 196 VDRVKKIKKGSITS 210

RESULT 27
F16P-PIG STANDARD; PRT; 337 AA.
ID F16P-PIG
AC P00636;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
DE 1-phosphohydrolyase) (FBPase).
GN FBP1 OR FBP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92212971; PubMed=1313579;
RA Williams M.K., Kantrowitz E.R.;
RT "Isolation and sequence analysis of the cDNA for pig kidney fructose
RT 1,6-bisphosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3080-3082(1992).
RN [2]
RP SEQUENCE OF 1-335.
RX MEDLINE=83117639; PubMed=6296821;
RA Marcus F., Edelstein I., Reardon I., Heinrichson R.L.;
RT "Complete amino acid sequence of pig kidney
RT fructose-1,6-bisphosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7161-7165(1982).
RN [3]
RP SEQUENCE OF 1-23 AND 43-60.
RX MEDLINE=83047209; PubMed=6291465;
RA McGregor J.S., Hannappel E., Xu G.-J., Pontremoli S., Horecker B.L.;
RT "Conservation of primary structure at the proteinase-sensitive site
RT of fructose 1,6-bisphosphatases.";
RL Arch. Biochem. Biophys. 217:652-664(1982).
RN [4]
RP SUBSTRATE-BINDING SITE, LIGANDS, AND REVIEW.
RX MEDLINE=82132308; PubMed=6277165;
RA Benkovic S.J., Demaille M.M.;
RT "Mechanism of action of fructose 1,6-bisphosphatase."


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FT HELIX 213 218
FT HELIX 221 231
FT TURN 234 235
FT STRAND 241 242
FT STRAND 244 244
FT HELIX 248 258
FT STRAND 261 264
FT STRAND 267 267
FT TURN 268 269
FT STRAND 270 270
FT TURN 271 272
FT STRAND 276 276
FT TURN 277 280

Query Match 50.7%; Score 37; DB 1; Length 337;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDRLVSIIRFGQHS 15
    :| | | | | | |
Db 196 VDRDVKKIKKGSIVS 210

RESULT 28
F16P-RAT STANDARD: PRT; 362 AA.
AC P19112; Q64594;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate
GN FBP1 OR FBP.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=89042197; PubMed=2847161;
RA El-Maghrabi M.R., Pltkis J., Marker A.J., Colosia A.D., D'Angelo G.,
RA Fraser B.A., Pltkis S.J.;
RT "cDNA sequence of rat liver fructose-1,6-bisphosphatase and evidence
RT for down-regulation of its mRNA by insulin."
RL Proc. Natl. Acad. Sci. U.S.A. 85:8430-8434(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96078844; PubMed=7589895;
RA Bettolotti R., Ammester L., Okayama H.;
RT Liver fructose-1,6-bisphosphatase cDNA: trans-complementation of
RT fission yeast and characterization of two human transcripts."
RL Differentiation 59:51-60(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=9115820; PubMed=1846613;
RA El-Maghrabi M.R., Lange A.J., Kummel L., Pltkis S.J.;
RT "The rat fructose-1,6-bisphosphatase gene. Structure and regulation
RT of expression."
RL J. Biol. Chem. 266:2115-2120(1991).
RN [4]
RP SEQUENCE OF 319-361.
RC TISSUE=Liver;
RA MEDLINE=8338340; PubMed=6305949;
RA Rittenhouse J., Chatterjee T., Marcus F., Reardon I., Heinrichson R.L.;
RT "Amino acid sequence of the COOH-terminal region of fructose-1,6-
RT bisphosphatase in relation to cyclic AMP-dependent
RT phosphorylation."
RL J. Biol. Chem. 258:7648-7653(1983).
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate + H(2)O = D-
CC fructose 6-phosphate + phosphate.
CC -1- ENZYME REGULATION: INHIBITED BY AMP, WHICH AFFECTS THE TURNOVER

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CC OF BOUND SUBSTRATE AND NOT THE AFFINITY FOR SUBSTRATE.
CC -1- PATHWAY: NECESSARY FOR, AND SPECIFIC TO, GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMOTETRAMER, WITH FOUR BINDING SITES
CC EACH FOR THE SUBSTRATE, FOR AMP, AND FOR DIVALENT METAL CATION
CC (THE GREATEST AFFINITY IS FOR ZINC).
CC -1- SIMILARITY: BELONGS TO THE FBPAE FAMILY.
CC -----
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CC -----
DR EMBL; J04113; AAA60739.1; -
DR EMBL; M86240; AAA86425.1; -
DR EMBL; M57284; AAA41131.1; -
DR EMBL; M57274; AAA41131.1; JOINED.
DR EMBL; M57279; AAA41131.1; JOINED.
DR EMBL; M57278; AAA41131.1; JOINED.
DR EMBL; M57282; AAA41131.1; JOINED.
DR EMBL; M57281; AAA41131.1; JOINED.
DR PIR; A1342; A31342.
DR HSSE; P00636; IEY.
DR InterPro; IPR000146; In_FB_phphatase.
DR Pfam; PF00316; FBPAE; 1.
DR PRINTS; PR00377; INFBPMPHTASE.
DR ProDom; PD001491; In_FB_phphatase; 1.
DR PROSITE; PS00124; FBPAE; 1.
KW Hydroxylase; Carbohydrate metabolism; Gluconeogenesis; Zinc;
KW Allosteric enzyme.
FT INIT_MET 0
FT BINDING 141 141 ALLOSTERIC REGULATION BY AMP (BY
FT ACT_SITE 274 274 SIMILARITY).
FT CONFLICT 147 147 P -> A (IN REF. 3).
SQ SEQUENCE 362 AA; 39478 MW; B07P61CDDCCIF2D CRC64;

Query Match 50.7%; Score 37; DB 1; Length 362;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDRLVSIIRFGQHS 15
    :| | | | | | |
Db 196 VDRDVKKIKKGSIVS 210

RESULT 29
AMCL_ORYZA /
ID AMCL_ORYZA STANDARD: PRT; 383 AA.
AC P27940;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alpha-amylase isozyme C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
GN glucanohydrolase) (Isozyme 1B).
GN AMYC OR AMY1B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indica-IR26; TISSUE=Leaf;
RA MEDLINE=92119260; PubMed=1731997;
RA Kim J.-K., Wu R.;
RT "Nucleotide sequence of a high-pi rice (Oryza sativa) -amylase gene."
RL Plant Mol. Biol. 18:399-402(1992).
RN [2]
RP SEQUENCE OF 1-50 FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;

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RX MEDLINE-91088278; PubMed-2263460;
RA Huang N., Koltzumi N., Reini S., Kodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylase genes."
RL Nucleic Acids Res. 18:7007-7014(1990).
CC -I- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -I- SUBUNIT: Monomer.
CC -I- TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEROMES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELLIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -I- CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO BE
CC FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
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CC -----
DR EMBL: X52240; CAA36485.1; -.
DR EMBL: M59350; AAA3893.1; -.
DR PIR: S19142; ALR20C.
DR HSP: P04063; IAVA.
DR Gramene; P27940; -.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; signal;
KW Multigene family.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 383 ALPHA-AMYLASE ISOZYME C.
SQ SEQUENCE 383 AA; 43254 MW; 7426BFE7C411B54 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 383;
Best Local Similarity 64.3%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDRLVSIRTRGOIH 14
   1: ||||| 1 1
DB 327 IECLVSRNRGOIH 340

RESULT 30
Y28_YEAST
ID Y28_YEAST STANDARD; PRT; 475 AA.
AC Q03790;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 52.6 kDa protein in IMPI-HL01 intergenic region.
GN YMR153W OR YMR520.02.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule G., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
CC -I- SIMILARITY: TO YEAST ASMA.

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CC -----
DR EMBL: 249705; CAA89789.1; -.
DR PIR: S54511; S54511.
DR SGD: S0004762; NRP53.
DR GO: GO:0005643; C:nuclear pore; IDA.
DR GO: GO:0000059; P:protein-nucleus import, docking; IPT.
DR Pfam: PF05172; MPN: 1.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52618 MW; 2E0E0C561D27E523 CRC64;

Query Match 50.7%; Score 37; DB 1; Length 475;
Best Local Similarity 53.8%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIRTRGOIHS 15
   1: :|||:|
DB 426 RSLFIRNRKGIHS 438

Search completed: August 29, 2003, 18:45:10
Job time : 11.8571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:40:26 ; Search time 36.8571 Seconds

(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-1

Perfect score: 73
Sequence: 1 IDRNVSRTRQIHS 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| 1 | 60 | 82.2 | 429 | 10 | Q40016 |
| 2 | 58 | 79.5 | 427 | 10 | Q03651 |
| 3 | 54 | 74.0 | 427 | 10 | Q40015 |
| 4 | 44 | 60.3 | 458 | 16 | Q40015 |
| 5 | 43 | 58.9 | 416 | 10 | Q92717 |
| 6 | 43 | 58.9 | 429 | 13 | Q8AJ06 |
| 7 | 43 | 58.9 | 544 | 17 | Q8AYB0 |
| 8 | 42 | 57.5 | 151 | 16 | Q9A204 |
| 9 | 42 | 57.5 | 345 | 4 | Q9NRA1 |
| 10 | 42 | 57.5 | 345 | 4 | Q9U122 |
| 11 | 42 | 57.5 | 666 | 17 | Q97UX8 |
| 12 | 40.5 | 55.5 | 343 | 16 | Q8KRC4 |
| 13 | 40 | 54.8 | 141 | 16 | Q8UR41 |
| 14 | 40 | 54.8 | 246 | 16 | Q9RWC1 |
| 15 | 40 | 54.8 | 416 | 10 | Q8GCR0 |
| 16 | 40 | 54.8 | 906 | 10 | Q8L0K4 |

| | | | | | | |
|----|------|------|------|----|--------|---------------------|
| 17 | 39.5 | 54.1 | 506 | 11 | Q9PA04 | Q9d4 mus musculus |
| 18 | 39 | 53.4 | 245 | 10 | Q9AT6 | Q9at6 arabidopsis |
| 19 | 39 | 53.4 | 272 | 10 | Q9S0R2 | Q9s0r2 arabidopsis |
| 20 | 39 | 53.4 | 284 | 3 | Q9C425 | Q9c425 ophiostoma |
| 21 | 39 | 53.4 | 409 | 4 | Q8TW13 | Q8tw13 homo sapien |
| 22 | 39 | 53.4 | 402 | 13 | Q8THU1 | Q8thu1 gallus galli |
| 23 | 39 | 53.4 | 443 | 3 | Q06098 | Q06098 saccharomyce |
| 24 | 39 | 53.4 | 443 | 11 | Q08P65 | Q08p65 mus musculus |
| 25 | 39 | 53.4 | 445 | 11 | Q9TX41 | Q9tx41 mus musculus |
| 26 | 39 | 53.4 | 467 | 16 | Q9K134 | Q9k134 streptomyce |
| 27 | 39 | 53.4 | 647 | 2 | Q9ABT8 | Q9abt8 salmonella |
| 28 | 38 | 52.1 | 137 | 16 | Q9AB88 | Q9ab88 caulobacter |
| 29 | 38 | 52.1 | 166 | 13 | Q9T8D5 | Q9t8d5 gallus galli |
| 30 | 38 | 52.1 | 177 | 16 | Q9T8D5 | Q9t8d5 gallus galli |
| 31 | 38 | 52.1 | 212 | 2 | Q69215 | Q69215 agrobacteri |
| 32 | 38 | 52.1 | 245 | 2 | Q9RIQ2 | Q9riq2 streptomyce |
| 33 | 38 | 52.1 | 270 | 3 | Q93874 | Q93874 curvularia |
| 34 | 38 | 52.1 | 737 | 10 | Q8S700 | Q8s700 oryza sativ |
| 35 | 38 | 52.1 | 1194 | 10 | Q9FKY7 | Q9fky7 arabidopsis |
| 36 | 37 | 50.7 | 142 | 16 | Q8YHL5 | Q8yhl5 bruceella me |
| 37 | 37 | 50.7 | 142 | 16 | Q8G095 | Q8g095 bruceella me |
| 38 | 37 | 50.7 | 143 | 16 | Q98N32 | Q98n32 rhizobium l |
| 39 | 37 | 50.7 | 155 | 17 | Q8TK54 | Q8tk54 methanosa |
| 40 | 37 | 50.7 | 168 | 13 | Q9T8D4 | Q9t8d4 gallus galli |
| 41 | 37 | 50.7 | 213 | 12 | Q8JUQ2 | Q8juq2 foot-and-mo |
| 42 | 37 | 50.7 | 223 | 3 | Q9C496 | Q9c496 bipolaris s |
| 43 | 37 | 50.7 | 250 | 3 | Q74141 | Q74141 bipolaris c |
| 44 | 37 | 50.7 | 250 | 3 | Q74150 | Q74150 bipolaris p |
| 45 | 37 | 50.7 | 250 | 3 | Q74157 | Q74157 bipolaris y |
| 46 | 37 | 50.7 | 250 | 3 | Q74159 | Q74159 bipolaris b |
| 47 | 37 | 50.7 | 250 | 3 | Q74153 | Q74153 bipolaris s |
| 48 | 37 | 50.7 | 250 | 3 | Q9UR11 | Q9ur11 bipolaris s |
| 49 | 37 | 50.7 | 250 | 3 | Q74145 | Q74145 bipolaris h |
| 50 | 37 | 50.7 | 250 | 3 | Q74155 | Q74155 bipolaris s |
| 51 | 37 | 50.7 | 250 | 3 | Q74156 | Q74156 bipolaris v |
| 52 | 37 | 50.7 | 250 | 3 | Q74143 | Q74143 cochllobolu |
| 53 | 37 | 50.7 | 250 | 3 | Q74149 | Q74149 bipolaris l |
| 54 | 37 | 50.7 | 250 | 3 | Q74142 | Q74142 bipolaris c |
| 55 | 37 | 50.7 | 250 | 3 | Q9URK8 | Q9urk8 bipolaris s |
| 56 | 37 | 50.7 | 250 | 3 | Q74160 | Q74160 bipolaris s |
| 57 | 37 | 50.7 | 250 | 3 | Q74138 | Q74138 bipolaris s |
| 58 | 37 | 50.7 | 250 | 3 | Q74152 | Q74152 bipolaris s |
| 59 | 37 | 50.7 | 250 | 3 | Q74152 | Q74152 bipolaris s |
| 60 | 37 | 50.7 | 250 | 3 | Q74146 | Q74146 curvularia |
| 61 | 37 | 50.7 | 250 | 3 | Q74144 | Q74144 bipolaris k |
| 62 | 37 | 50.7 | 250 | 3 | Q74151 | Q74151 cochllobolu |
| 63 | 37 | 50.7 | 250 | 3 | Q74158 | Q74158 bipolaris p |
| 64 | 37 | 50.7 | 250 | 3 | Q74148 | Q74148 bipolaris z |
| 65 | 37 | 50.7 | 250 | 3 | Q74140 | Q74140 bipolaris n |
| 66 | 37 | 50.7 | 250 | 3 | Q74154 | Q74154 bipolaris s |
| 67 | 37 | 50.7 | 250 | 3 | Q74147 | Q74147 bipolaris c |
| 68 | 37 | 50.7 | 256 | 5 | Q9NCB5 | Q9ncb5 trllobium c |
| 69 | 37 | 50.7 | 267 | 3 | Q93802 | Q93802 altermaria |
| 70 | 37 | 50.7 | 267 | 3 | Q42693 | Q42693 cochllobolu |
| 71 | 37 | 50.7 | 267 | 3 | Q8JRT3 | Q8jrt3 bipolaris o |
| 72 | 37 | 50.7 | 267 | 3 | Q8JZM1 | Q8jzm1 curvularia |
| 73 | 37 | 50.7 | 271 | 3 | Q87025 | Q87025 colletotric |
| 74 | 37 | 50.7 | 277 | 5 | Q9S0G7 | Q9sg07 caenorhabdi |
| 75 | 37 | 50.7 | 328 | 15 | Q9EE70 | Q9ee70 human immu |
| 76 | 37 | 50.7 | 329 | 15 | Q9EE70 | Q9ee70 human immu |
| 77 | 37 | 50.7 | 337 | 6 | Q77657 | Q77657 sus scrofa |
| 78 | 37 | 50.7 | 412 | 10 | Q9SGS0 | Q9sgs0 arabidopsis |
| 79 | 37 | 50.7 | 413 | 10 | Q8LRG1 | Q8lrg1 arabidopsis |
| 80 | 37 | 50.7 | 413 | 10 | Q9M6R9 | Q9m6r9 malus domes |
| 81 | 37 | 50.7 | 437 | 11 | Q8THU5 | Q8thu5 mus musculus |
| 82 | 37 | 50.7 | 444 | 2 | Q9TX46 | Q9tx46 mus musculus |
| 83 | 37 | 50.7 | 496 | 16 | Q9RWT6 | Q9rwt6 pseudomonas |
| 84 | 37 | 50.7 | 570 | 3 | Q9SE29 | Q9se29 oryza sativ |
| 85 | 37 | 50.7 | 615 | 16 | Q9KX20 | Q9kx20 neurospora |
| 86 | 37 | 50.7 | 615 | 16 | Q9KX20 | Q9kx20 neurospora |
| 87 | 37 | 50.7 | 615 | 16 | Q9KX20 | Q9kx20 neurospora |
| 88 | 37 | 50.7 | 710 | 6 | Q9KX62 | Q9kx62 ceratopline |
| 89 | 37 | 50.7 | 743 | 5 | Q8WPU5 | Q8wpu5 drosophila |
| 90 | 37 | 50.7 | 989 | 5 | Q8ML20 | Q8ml20 drosophila |

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90      37      50.7      2514      5      Q9Y061      caenorhabdi
91      37      50.7      2531      5      Q22258      caenorhabdi
92      37      50.7      4753      16      Q8PI13      xanthomonas
93      36.5      50.0      441      5      Q9VW38      drosophila
94      36.5      50.0      441      5      Q8SVU7      drosophila
95      36      49.3      83      16      Q9A931      caulobacter
96      36      49.3      156      2      Q8RS47      uncultured
97      36      49.3      159      2      Q9JMY7      listeria mo
98      36      49.3      161      13      Q9JMF2      esox lucius
99      36      49.3      165      2      Q9JMW0      listeria mo
100     36      49.3      168      2      Q9JMY9      listeria mo

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ALIGNMENTS

RESULT 1
Q40016 PRELIMINARY; PRT; 429 AA.

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AC Q40016 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Barley (H. vulgare) alpha-amylase 1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
RT barley."
RL Plant Mol. Biol. 9:3-17(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Muthukrishnan S.;
RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR EMBL; M17125; AAA32926.1; -.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 429 AA: 47970 MW: 4E7B8B741C944095 CRC64;

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Query Match 82.2%; Score 60; DB 10; Length 429;
Best Local Similarity 86.7%; Pred. No. 0.0081;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
Db 360 IDRLVSIRTRGOIHS 374

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RESULT 2
ID Q03651 PRELIMINARY; PRT; 427 AA.
AC Q03651
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha-amylase precursor (Ec 3.2.1.1).
GN AMY46.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Himalaya;

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RX MEDLINE=89066691; PubMed=3264283;
RA Knutshed B., Rogers J.C.;
RT "Barley alpha-amylase genes. Quantitative comparison of steady-state
RT mRNA levels from individual members of the two different families
RT expressed in aleurone cells."
RL J. Biol. Chem. 263:18953-18960(1988).
DR EMBL; J04202; AAA98615.1; -.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 25
FT CHAIN 26 427
SQ SEQUENCE 427 AA: 47456 MW: 5A7496B9B6643824 CRC64;

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Query Match 79.5%; Score 58; DB 10; Length 427;
Best Local Similarity 86.7%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
Db 358 IDRLVSIRTRGOIHS 372

RESULT 3
Q40015 PRELIMINARY; PRT; 427 AA.

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AC Q40015
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Barley (H. vulgare) alpha-amylase 1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
RT barley."
RL Plant Mol. Biol. 9:3-17(1987).
RN [2]
RP SEQUENCE FROM N.A.
RA Muthukrishnan S.;
RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR EMBL; M17126; AAA32925.1; -.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
SQ SEQUENCE 427 AA: 47402 MW: D21BA12EAB5F3534 CRC64;

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Query Match 74.0%; Score 54; DB 10; Length 427;
Best Local Similarity 73.3%; Pred. No. 0.11;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 IDRLVSIRTRGOIHS 15
Db 358 IDRLVSIRTRGOIHS 372

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RESULT 4
ID Q92717 PRELIMINARY; PRT; 458 AA.
AC Q92717
DT 01-MAY-1999 (TREMBlrel. 10, Created)

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RP SEQUENCE FROM N.A.
RX MEDLINE-214763; PubMed-11297552;
RA Galberston D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
RT "Platelet-derived Growth Factor C (PDGF-C), a Novel Growth Factor That
RT Binds to PDGF alpha and beta Receptor."
RT J Biol Chem 276:27406-27414(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF091434; AF000491; -.
DR EMBL: AB033831; BAB03266.1; -.
DR EMBL: AF260738; AAK51637.1; -.
DR InterPro: IPR000859; CUB_domain.
DR InterPro: IPR000772; PD_growth_factor.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 57.5%; Score 42; DB 4; Length 345;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 2 DRLVLSIRTRQIHS 15
DB 47 ERLIVSTNGSIHS 60

RESULT 11
O97UX8 PRELIMINARY; PRT; 666 AA.
AC O97UX8;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acetyl-CoA synthetase (Acetate CoA ligase) (acsA-9) (EC 6.2.1.1).
GN ACSA-9 OR SSO2863.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus;
NCBI_TaxID-2287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-2132296; PubMed-11427726;
RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awaiz M.J., Chan-Welher C.C.Y., Clausen I.G., Curtis B.A.,
RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.K.,
RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Regan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
RL EMBL: AE006879; AAK42970.1; -.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMP-BINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 666 AA; 75799 MW; E2779A7118B7C2C5 CRC64;

Query Match 57.5%; Score 42; DB 17; Length 666;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 DRLVLSIRTRQIHS 15
DB 19 LRLVLSITTKIHS 33

RESULT 12
O8KDC4 PRELIMINARY; PRT; 343 AA.
AC O8KDC4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein CT1130.
GN CT1130.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID-1097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-TLS / ATCC 49652 / DSM 12025;
MEDLINE-22103685; PubMed-12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamthavan J., Khouri H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RT Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
RL EMBL: AE012874; AAM72363.1; -.
DR TIGR: CT1130; -.
DR InterPro: IPR002729; DUF48.
DR Pfam: PF01867; DUF48; 1.
DR Pfam: PD008695; DUF48; 1.
DR TIGRPMAS: TIGR00287; TIGR00287; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 343 AA; 38756 MW; 9DF5B16504974866 CRC64;

Query Match 55.5%; Score 40.5; DB 16; Length 343;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 2 DRLVLSIRTRQIHS 15
DB 257 DRLVLSLNRQIHA 271

RESULT 13
O8UE41 PRELIMINARY; PRT; 141 AA.
AC O8UE41;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 50S ribosomal protein L17.
GN RPLO OR ATU1922 OR AGR_C3516.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobaceae; Rhizobium.
OX NCBI_TaxID-176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21608550; PubMed-11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Woo L.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutyavin T., Levy R., Li M.-T., McClelland E., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Xeo H., Tao Y., Biddle P., Jung M., Kresan P., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-X., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.F., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens

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RT C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Ourfolllo B., Goldman B.S., Cao Y., Askenezai M., Halling C., Mullin L.,
 RA Houmiel K., Gordon J., Vaudin M., Iatchouk O., Bpp A., Liu F.,
 RA Wollam C., Allinger M., Doughly D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009146; AAL42918.1;
 DR EMBL: AE008111; AAK87683.1;
 DR InterPro: IPR000456; Ribosomal_L17.
 DR Pfam: PF01196; Ribosomal_L17; 1.
 DR Prodom: PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS: TIGR00059; L17; 1.
 DR PROSITE: PS01167; RIBOSOMAL_L17; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 141 AA; 15395 MW; CD37B5D4E2D79D35 CRC64;

Query Match 54.8%; Score 40; DB 16; Length 141;
 Best Local Similarity 40.0%; Pred. NO. 15;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDRLVSIPTRGQIHS 15
 Db 48 VERLVTIGKRGDLHA 62

RESULT 14
 Q9RMC1 PRELIMINARY; PRT; 246 AA.
 ID Q9RMC1;
 AC Q9RMC1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE RNA methyltransferase, TRMh family.
 GN DR0748.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-thermus; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 NC NCB1_TaxID=1299;
 RP NCBI TaxID=1299;
 RC [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vanathavan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1."
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001930; AAF10325.1;
 DR TIGR: DR0748;
 DR InterPro: IPR004441; rRNA_methyl_3.
 DR InterPro: IPR001537; Spou_methylase.
 DR Pfam: PF00588; Spou_methylase; 1.
 DR Prodom: PD001243; Spou_methylase; 1.
 DR TIGRFAMS: TIGR00186; rRNA_methyl_3; 1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 246 AA; 26179 MW; 3E1827C743CE3A8 CRC64;

Query Match 54.8%; Score 40; DB 16; Length 246;
 Best Local Similarity 64.3%; Pred. NO. 27;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 DRLVSIPTRGQIHS 15
 Db 208 DVLVSIPTRGQVGS 221

RESULT 15
 ID Q8GUR0 PRELIMINARY; PRT; 416 AA.
 AC Q8GUR0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1).
 OS Musa acuminata (Banana).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
 OC Musa.
 NC NCB1_TaxID=4641;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nandica; TISSUE=leaf;
 RA Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
 RT "Sequencing and molecular characterization of a banana alpha-amylase
 RT gene."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY171068; AAO11776.1;
 DR Signal; Hydrolase; Glycosidase.
 FT SIGNAL 1 15 POTENTIAL.
 FT CHAIN 16 416 ALPHA-AMYLASE.
 SQ SEQUENCE 416 AA; 46558 MW; 7D5EC630F221915 CRC64;

Query Match 54.8%; Score 40; DB 10; Length 416;
 Best Local Similarity 60.0%; Pred. NO. 47;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IDRLVSIPTRGQIHS 15
 Db 347 ITRLAKTRTRNGIHS 361

RESULT 16
 Q8LQK4 PRELIMINARY; PRT; 906 AA.
 ID Q8LQK4;
 AC Q8LQK4;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative alpha-amylase.
 GN B1131B07.22
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartodeae; Oryzaceae; Oryza.
 NC NCB1_TaxID=39947;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 RT clone:B1131B07."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003408; BAB93360.1;
 DR Gramene; Q8LQK4;
 DR InterPro: IPR006047; Alpha-amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amyy; 1.
 SQ SEQUENCE 906 AA; 101641 MW; AEFD187910DD55C5 CRC64;

Query Match 54.8%; Score 40; DB 10; Length 906;

Best Local Similarity 57.1%; Pred. No. 1,le02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 DRLVSIRTRG 14
| : : : : :
Db 837 IAKLISIRTRG 850

RESULT 17
O9DA04 PRELIMINARY; PRT; 506 AA.
AC O9DA04; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 1700003E16RIK protein.
GN 1700003E16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flieschman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Offito T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata J., Storch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL, AK005628, BAB24157.1, -;
DR MOP, MGI1919087, 170003E16RIK.
SQ SEQUENCE 506 AA; 35305 MW; 1AA360BCEDA709 CRC64;
Query Match 54.1%; Score 39.5; DB 11; Length 506;
Best Local Similarity 57.1%; Pred. No. 72;
Matches 8; Conservative 5; Mismatches 0; Indels 1; Gaps 1;
OY 2 DRLVSIRTRG 15
| : : : : :
Db 189 DRL-SIASKGOLHS 201
RESULT 18
O94AT6 PRELIMINARY; PRT; 245 AA.
AC O94AT6; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 22, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase (Fragment).
GN AT3G04000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carlinici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Saito M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.; Full length cDNA clones."
RT "Arabidopsis (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AY045807; AAK76481.2; -;
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 245 AA; 25906 MW; CE98FC78C53841P5 CRC64;

Query Match 53.4%; Score 39; DB 10; Length 245;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 2 DRLVSIRTRG 11
| : : : : :
Db 105 DRLVSIRTRG 114
RESULT 19
O9SOR2 PRELIMINARY; PRT; 272 AA.
AC O9SOR2; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative short-chain type dehydrogenase/reductase.
GN T1118.11 OR AT3G04000
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Beilto M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T1118 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
DR EMBL: AC011698; AAF05859.1; -;
DR EMBL: BT002321; AAN6154.1; -;
DR HSSP: Q12634.1YBV.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 272 AA; 28434 MW; 1F0542EF7C599276 CRC64;

Query Match 53.4%; Score 39; DB 10; Length 272;
Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DRLVSIRTRG 11
 |||:|: |||
 DB 132 DRLISVNRG 141

RESULT 20
 09C425 PRELIMINARY; PRT; 284 AA.

ID 09C425
 AC 09C425;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Reductase.
 OS Ophiostoma floccosum.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Ophiostomatales; Ophiostomataceae; Ophiostoma.
 NCBI_TaxID=104300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang H., Breuil C.;
 RT "A second reductase gene involved in melanin biosynthesis from the
 RT sapstaining fungus, Ophiostoma floccosum.";
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 CC (SBR) FAMILY.
 DR EMBL; AF317668; AK07185.1; -.
 DR HSSP; Q12634; 1YBY.
 DR InterPro: IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 284 AA; 30141 MW; F35E0E0604DCE2 CRC64;

Query Match 53.4%; Score 39; DB 3; Length 284;
 Best Local Similarity 63.6%; Pred. No. 49;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DRLVSIRTRG 12
 ||:|: |||
 DB 134 DRLFSVNRG 144

RESULT 21
 081W13 PRELIMINARY; PRT; 402 AA.

ID 081W13
 AC 081W13;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to nuclear receptor subfamily 1, group H, member 3.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC041172; AAH41172.1; -.
 KW Receptor.
 SQ SEQUENCE 402 AA; 45691 MW; 78EA53CFB2358E7 CRC64;

Query Match 53.4%; Score 39; DB 4; Length 402;
 Best Local Similarity 53.8%; Pred. No. 71;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQHS 15
 :|||:|: :||
 DB 365 KLVSIIRTRLSVSHS 377

RESULT 22
 08JHU1 PRELIMINARY; PRT; 409 AA.

ID 08JHU1
 AC 08JHU1;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Liver x receptor.
 GN LXR.
 OS Gallus gallus (Chicken).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-22162479; PubMed-12045201;
 RA Handschin C., Podvinet M., Amherd R., Looser R., Ourlin J.C.,
 RA Meyer U.A.;
 RT "Cholesterol and Bile Acids Regulate Xenosensor Signaling in Drug-
 RT mediated Induction of Cytochromes P450.";
 RL J. Biol. Chem. 277:29561-29567(2002).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
 DR EMBL; AF492498; AA090897.1; -.
 DR InterPro: IPR000536; Hormone_rec_11g.
 DR InterPro: IPR001723; Stdrhm_receptor.
 DR InterPro: IPR001628; Znfc4steroid.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHOMNER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR Prodom; PD000035; Znfc4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; ZnfC4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 409 AA; 47056 MW; 156C9FAB92A46587 CRC64;

Query Match 53.4%; Score 39; DB 13; Length 409;
 Best Local Similarity 53.8%; Pred. No. 72;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RLVSIIRTRGQHS 15
 :|||:|: :||
 DB 372 KLVSIIRTRLSVSHS 384

RESULT 23
 006098 PRELIMINARY; PRT; 443 AA.

ID 006098
 AC 006098;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to protein kinases GCN2.
 GN ISR1 OR P8283.9 OR YPR106W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C.

RX MEDLINE-97313271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansgore W.,
 RA Araujo R., Aparicio A., Bartell B., Badcock K., Benes V., Bolstein D.,
 RA Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
 RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
 RA Delius H., Dipolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative membrane protein.
 GN SCO2356 OR SCC8A.14.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 NC NCB1_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145.
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nucleic Acids Res. 30(14):4172-4182 (2002).
 DR EMBL; AL939112; CAB92832.1; -.
 KW Complete proteome.
 SQ SEQUENCE 467 AA; 51174 MW; CD8EB236C6A3C4E CRC64;

Query Match 53.4%; Score 39; DB 16; Length 467;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 RLVSIRTRGQ 12
 |||||
 DB 279 RLVSIRTRGQ 288

RESULT 27
 Q9ADT8 PRELIMINARY; PRT; 847 AA.
 AC Q9ADT8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative subtilisin proteinase-like protein.
 GN S025.
 OS Salmonella enterica subsp. enterica serovar Typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCB1_TaxID=90371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-96-5227;
 RX MEDLINE=21429247; PubMed=11544236;
 RA Boyd D., Peters G.A., Cloeckaert A., Boumediene K.S.,
 RA Chaslus-Dancla E., Imberechts H., Mulvey M.R.;
 RT "Complete Nucleotide Sequence of a 43-Kilobase Genomic Island
 Associated with the Multidrug Resistance Region of *Salmonella enterica*
 RT Serovar Typhimurium DT104 and Its Identification in Phage Type DT120
 RT and Serovar Agona";
 RT J. Bacteriol. 183:5725-5732(2001).
 DR EMBL; AF261825; AAK02042.1; -.
 DR InterPro; IPR000209; Peptidase_S8.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 SQ SEQUENCE 847 AA; 95237 MW; 8B8D2843C2E21B93 CRC64;

Query Match 53.4%; Score 39; DB 2; Length 847;
 Best Local Similarity 77.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 ITRGQIHS 15
 :|||||

DB 762 LTRGSIHS 770

RESULT 28
 Q9A8S8 PRELIMINARY; PRT; 137 AA.
 AC Q9A8S8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Ribosomal protein L17.
 GN CCL273.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCB1_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RX MEDLINE=21173658; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Pladke N.D., Ely B.,
 RA Debay R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Uetzelberg S.L., Tran K., Wolf A., Yamathayan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005802; AAK23254.1; -.
 DR TIGR; CCL273; -.
 DR InterPro; IPR000456; Ribosomal_L17.
 DR Pfam; PF01196; Ribosomal_L17; 1.
 DR PRODOM; PD004277; Ribosomal_L17; 1.
 DR TIGRFAMS; TIGR00059; L17; 1.
 DR PROSITE; PS01167; RIBOSOMAL_L17; 1.
 KW Complete proteome.
 SQ SEQUENCE 137 AA; 15326 MW; F9F0EC66F33E6FE4 CRC64;

Query Match 52.1%; Score 38; DB 16; Length 137;
 Best Local Similarity 33.3%; Pred. No. 36;
 Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 IDRVSIRTRGQIHS 15
 ::||::||:|
 DB 48 VERLVTIAKRGDLHA 62

RESULT 29
 Q91BD3 PRELIMINARY; PRT; 166 AA.
 AC Q91BD3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
 GN FBP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCB1_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Tillmann H., Eschrich K.;
 RT "The gene duplication leading to present-day liver and muscle type
 RT genes of fructose-1,6-bisphosphatase occurred prior to the divergence
 RT of mammalia and amphibia."; EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ276213; CAB99413.1; -.
 DR HSSP; P00636; IFBP.
 DR InterPro; IPR000146; In_FB_phphatase.

DR Pfam: PF00316; Fbpase; 1.
 DR ProDom: PD001491; In_FB_phphatase; 1.
 KM Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 166 166
 SQ SEQUENCE 166 AA; 18234 MW; E804E1EE3534C0E CRC64;

Query Match 52.1%; Score 38; DB 13; Length 166;
 Best Local Similarity 46.7%; Pred. No. 44;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 DRLVSIRTCQIHS 15
 :|||:|:|:|:|:|:|
 Db 115 VDRDVKIRKKGKLYS 129

RESULT 30

Q8G322 PRELIMINARY; PRT: 177 AA.
 AC Q8G322;
 DT 01-MAR-2003 (TREMBLrel, 23, Created)
 DT 01-MAR-2003 (TREMBLrel, 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel, 23, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ OR BL1607.
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NC 2705;
 RX MEDLINE=2228497; PubMed=12381787;
 RA Schell M.A., Karmali-Mou M., Shet B., Vilanova D., Berger B.,
 RA Besi G., Zahnen M.-C., Desiere F., Bork P., Delley M.,
 RA Pridmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL: AE014794; AAN25396.1; -;
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 177 AA; 19121 MW; 52F9BD7C8F881F59 CRC64;

Query Match 52.1%; Score 38; DB 16; Length 177;
 Best Local Similarity 42.9%; Pred. No. 47;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 DRLVSIRTCQIHS 15
 :|||:|:|:|:|:|:|
 Db 49 ERLITFAKRGDLHS 62

Search completed: August 29, 2003, 18:46:44
 Job time : 39.8571 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:35:10 ; Search time 30.5714 Seconds

(without alignments)
51.920 Million cell updates/sec

Title: US-09-830-876-2

Perfect score: 61

Sequence: 1 CRDDPRPADG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A.Geneseq_19jun03.*
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2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 61 | 100.0 | 10 | 21 | AAV93372 |
| 2 | 61 | 100.0 | 425 | 21 | AAV93374 |
| 3 | 44 | 72.1 | 189 | 21 | AAAB16296 |
| 4 | 41.5 | 68.0 | 428 | 21 | AAAB12798 |
| 5 | 41.5 | 68.0 | 428 | 22 | AAAS0251 |
| 6 | 41.5 | 68.0 | 428 | 22 | AAAB97245 |
| 7 | 41.5 | 68.0 | 429 | 16 | AAAB76520 |
| 8 | 41.5 | 68.0 | 433 | 15 | AAAS5130 |
| 9 | 41.5 | 68.0 | 434 | 14 | AAAB32987 |

| | | | | | |
|----|------|------|------|----|-----------|
| 10 | 41.5 | 68.0 | 434 | 18 | AAAB1871 |
| 11 | 41.5 | 68.0 | 434 | 20 | AAV01375 |
| 12 | 41.5 | 68.0 | 434 | 21 | AAAB4383 |
| 13 | 41.5 | 68.0 | 434 | 21 | AAAB87992 |
| 14 | 41 | 67.2 | 215 | 11 | AAAB07669 |
| 15 | 39 | 63.9 | 594 | 22 | AAAB59190 |
| 16 | 38 | 62.3 | 435 | 22 | AAAS0253 |
| 17 | 38 | 62.3 | 435 | 22 | AAAB97247 |
| 18 | 38 | 62.3 | 1036 | 20 | AAAB81063 |
| 19 | 38 | 62.3 | 1036 | 22 | AAAB59323 |
| 20 | 38 | 62.3 | 1036 | 22 | AAAB28647 |
| 21 | 37 | 60.7 | 17 | 11 | AAAB07159 |
| 22 | 37 | 60.7 | 17 | 11 | AAAB07159 |
| 23 | 37 | 60.7 | 17 | 11 | AAAB07159 |
| 24 | 37 | 60.7 | 118 | 14 | AAAB41885 |
| 25 | 37 | 60.7 | 346 | 24 | AAAB71159 |
| 26 | 37 | 60.7 | 413 | 23 | AAAB41533 |
| 27 | 37 | 60.7 | 452 | 21 | AAAB96343 |
| 28 | 37 | 60.7 | 593 | 14 | AAAB91957 |
| 29 | 37 | 60.7 | 593 | 14 | AAAB48673 |
| 30 | 37 | 60.7 | 593 | 14 | AAAB85475 |
| 31 | 37 | 60.7 | 593 | 23 | AAAB20521 |
| 32 | 37 | 60.7 | 771 | 22 | AAAB07869 |
| 33 | 37 | 60.7 | 845 | 22 | AAAB07869 |
| 34 | 37 | 60.7 | 886 | 21 | AAAB33370 |
| 35 | 37 | 60.7 | 926 | 22 | AAAB83370 |
| 36 | 37 | 60.7 | 1281 | 22 | AAAB10610 |
| 37 | 37 | 60.7 | 1617 | 22 | AAAB07870 |
| 38 | 37 | 60.7 | 1691 | 22 | AAAB10609 |
| 39 | 37 | 60.7 | 1691 | 22 | AAAB07863 |
| 40 | 36 | 59.0 | 224 | 22 | AAAB07870 |
| 41 | 36 | 59.0 | 246 | 22 | AAAB35390 |
| 42 | 36 | 59.0 | 255 | 22 | AAAB34668 |
| 43 | 36 | 59.0 | 255 | 22 | AAAB38492 |
| 44 | 36 | 59.0 | 349 | 11 | AAAB07668 |
| 45 | 36 | 59.0 | 2432 | 22 | AAAB06023 |
| 46 | 36 | 59.0 | 4660 | 22 | AAAB23830 |
| 47 | 36 | 59.0 | 4765 | 24 | AAAB32730 |
| 48 | 35 | 58.2 | 4854 | 22 | AAAB06027 |
| 49 | 35 | 58.2 | 4854 | 22 | AAAB93962 |
| 50 | 35 | 57.4 | 98 | 23 | AAAB43583 |
| 51 | 35 | 57.4 | 98 | 21 | AAAB27196 |
| 52 | 35 | 57.4 | 98 | 22 | AAAB54151 |
| 53 | 35 | 57.4 | 114 | 22 | AAAB94845 |
| 54 | 35 | 57.4 | 129 | 20 | AAAB25030 |
| 55 | 35 | 57.4 | 196 | 22 | AAAB25030 |
| 56 | 35 | 57.4 | 196 | 22 | AAAB70785 |
| 57 | 35 | 57.4 | 196 | 21 | AAAB08436 |
| 58 | 35 | 57.4 | 196 | 22 | AAAB43325 |
| 59 | 35 | 57.4 | 196 | 22 | AAAB45893 |
| 60 | 35 | 57.4 | 223 | 21 | AAAB43324 |
| 61 | 35 | 57.4 | 223 | 21 | AAAB08435 |
| 62 | 35 | 57.4 | 226 | 11 | AAAB05907 |
| 63 | 35 | 57.4 | 226 | 13 | AAAB25332 |
| 64 | 35 | 57.4 | 226 | 13 | AAAB30015 |
| 65 | 35 | 57.4 | 226 | 15 | AAAB46496 |
| 66 | 35 | 57.4 | 226 | 15 | AAAB46496 |
| 67 | 35 | 57.4 | 227 | 11 | AAAB05908 |
| 68 | 35 | 57.4 | 243 | 20 | AAAB05908 |
| 69 | 35 | 57.4 | 306 | 21 | AAAB68243 |
| 70 | 35 | 57.4 | 306 | 21 | AAAB52897 |
| 71 | 35 | 57.4 | 306 | 22 | AAAB58658 |
| 72 | 35 | 57.4 | 554 | 22 | AAAB92535 |
| 73 | 35 | 57.4 | 554 | 22 | AAAB92535 |
| 74 | 35 | 57.4 | 1264 | 18 | AAAB62419 |
| 75 | 35 | 57.4 | 1864 | 18 | AAAB26602 |
| 76 | 34 | 55.6 | 434 | 22 | AAAB10469 |
| 77 | 34 | 55.7 | 63 | 22 | AAAB41954 |
| 78 | 34 | 55.7 | 87 | 22 | AAAB49827 |
| 79 | 34 | 55.7 | 94 | 22 | AAAB17948 |
| 80 | 34 | 55.7 | 117 | 24 | AAAB71160 |
| 81 | 34 | 55.7 | 127 | 24 | AAAB60662 |
| 82 | 34 | 55.7 | 132 | 22 | AAAB22550 |

Rice alpha-amylase
O. sativa alpha-am
Rice alpha-amylase
Rice alpha-amylase
Partial alpha-amyl
Drosophila melanog
Rice alpha-amylase
Alpha-amylase rela
Mulin acid sequenc
Drosophila melanog
Synthetic Nerve gr
NGF, chicken. Gal
Granulin E. Homo
Chicken mature NGF
Human DTRP protei
Human ovarian canc
Human cytoskeleton
Granulin sequence.
Human GP88 autocr
Human granuln/epi
Novel human protei
Novel human protei
Human ORFX ORF264
NOV14 protein sequ
Human novel KIAI12
Human novel KIAI12
Novel human protei
Human novel KIAI12
Novel human protei
Hemophilus influe
E. coli cellular p
Salmonella typhi C
Partial alpha-amyl
Novel human diago
Human EST encoded
HRCR3 proteoic Un
Novel human diago
Arabidopsis thalian
Zea mays protein f
Protonibacterium
Protonibacterium
Human protein sequ
T. gondii Immuno
S. cerevisiae apopt
Arabidopsis thalia
Arabidopsis thalia
Protonibacterium
Arabidopsis thalia
Arabidopsis thalia
Rat neuronal growt
Sequence encoded b
Rat GAP-43. Rattu
Rat GAP-43. Rattu
Rat GAP-43. Rattu
C. ensiformis chit
Murine class I mol
Murine class I mol
C glutamicum prote
Corynebacterium gl
Protonibacterium
Tylactone synthase
Rice alpha-amylase
Protonibacterium
Protonibacterium
Novel human diago
Xenopus mature NGF
Drosophila melanog
Novel human diago

| | |
|-----------------------|--|
| AA161296 | standard; Protein: 189 AA. |
| XX | |
| AC | AA161296; |
| XX | |
| DT | 31-OCT-2000 (first entry) |
| XX | |
| DE | Eucalyptus grandis amylase protein sequence SEQ ID NO:82. |
| XX | |
| KM | Eucalyptus grandis; plus radlta; Monterey pine; modification; |
| KM | plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; |
| XX | transgenic plant. |
| XX | |
| OS | Eucalyptus grandis. |
| XX | |
| XX | MO200022092-A2. |
| PD | 20-APR-2000. |
| XX | |
| PF | 08-OCT-1999; 99WO-N200169. |
| XX | |
| PR | 13-OCT-1998; 98US-0170862. |
| PR | 11-AUG-1999; 99US-0148426. |
| XX | |
| PA | (GENE-) GENESIS RES & DEV CORP LTD. |
| PA | (FLET-) FLETCHER CHALLENGE FORESTS LTD. |
| XX | |
| PI | Bloksberg LN; |
| DR | WPI: 2000-339328/29. |
| DR | N-PSDB; AA67103. |
| XX | |
| PT | New genes encoding proteins involved in a plant polysaccharide |
| PT | biosynthetic pathway, useful for modulating or altering the |
| PT | polysaccharide content, composition or structure of the plant - |
| XX | |
| PS | Claim 17; Page 77; 30pp; English. |
| XX | |
| CC | The present invention describes isolated polynucleotides (PN) comprising |
| CC | a sequence selected from one of 835 nucleotide sequences given in |
| CC | AA67073 to AA67907, their (reverse) complements, sequences producing |
| CC | an expectation (E) value of 0.01 or less compared to the 835 sequences, |
| CC | sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the |
| CC | 835 sequences or sequences that are degenerately equivalent or allelic |
| CC | to the 835 sequences. The polynucleotides are used to modify the |
| CC | activity of a polypeptide involved in a polysaccharide biosynthetic |
| CC | pathway in the plant. They are especially used to modulate or alter the |
| CC | polysaccharide content, composition or structure of the plant. AA16268 |
| CC | to AA16340 are proteins encoded by some of the polynucleotide sequence |
| CC | given in the present invention. |
| XX | |
| XX | |
| SQ | Sequence 189 AA: |
| XX | |
| Query Match | 72.1%; Score 44; DB 21; Length 189; |
| Best Local Similarity | 70.0%; Pred. No. 7.5; |
| Matches | 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0; |
| Oy | 1 CRDDRPYADG 10 |
| Db | :: |
| | 142 CRDDTEYS DG 151 |
| RESULT 4 | |
| AA1612798 | |
| ID | AA1612798 standard; Protein: 428 AA. |
| XX | |
| AC | AA1612798; |
| XX | |
| DT | 23-NOV-2000 (first entry) |
| XX | |
| DE | Rice alpha-Amy7-C protein SEQ ID NO:2. |
| XX | |
| XX | Rice; alpha-Amy6-C; alpha-Amy7-C; alpha-Amy8-C; alpha-Amy10-C; |

| | |
|----------|--|
| XX | gene expression; promoter region; alpha-amylase; transgenic plant. |
| XX | Oryza sativa. |
| OS | JP2000157080-A. |
| PN | 13-JUN-2000. |
| FD | 04-NOV-1993; 99UP-0356560. |
| XX | 05-NOV-1992; 92UP-0321274. |
| PR | 04-NOV-1993; 93UP-0297607. |
| XX | (NASC-) NAT SCI COUNCIL. |
| PA | WPI: 2000-468171/41. |
| DR | N-PSDB; AAA72947. |
| XX | A gene expression system containing the promoter region of |
| PT | alpha-amylase gene, useful for mass production of a desired gene |
| PT | product in a plant host cell |
| XX | Example 1; Page 27-30; 39pp; Japanese. |
| PS | The present invention describes a gene expression system containing the |
| CC | promoter region of an alpha-amylase gene. Also described is a method for |
| CC | preparing a transgenic rice plant comprising: (1) infecting Agrobacterium |
| CC | into an unmutated embryo of a rice plant; (2) simultaneously culturing |
| CC | the embryo with a suspended culture of a dicotyledon during the |
| CC | transforming step; (3) growing the transformed embryo to a callus in a |
| CC | selective medium containing a plant growth hormone; and (4) regenerating |
| CC | the callus into roots and sprouts in a regeneration medium. The method can |
| CC | be used for mass production of a desired gene product in a plant host |
| CC | cell. The present sequence represents the rice alpha-amylase protein, |
| XX | which is used in an example from the present invention. |
| XX | Sequence 428 AA: |
| SQ | |
| QY | I CRDREPYADG 10 Db 149 CRDD-PYGDG 157 |
| RESULT 5 | |
| ID | AAAM50251 standard; Protein: 428 AA. |
| AC | AAAM50251; |
| XX | 21-JAN-2002 (first entry) |
| DT | Rice alpha-amylase (alpha-Amyl-C gene product). |
| DE | Alpha-amylase; promoter; rice; transgenic plant; angiosperm; |
| KW | monocot; cereal; brewing. |
| XX | Oryza sativa. |
| OS | Key |
| XX | Peptide 1..23 Location/Qualifiers |
| FT | /Label= Signal_peptide |
| FT | Protein 26..428 /Label= Mature_protein |
| FN | US6288302-B1. |
| PD | 11-SEP-2001. |
| XX | 04-MAY-1998; 98US-0072917. |

| | | | |
|-----------------------|---|---------------|--|
| XX | 04-NOV-1992: | 92US-0973324. | |
| XX | 01-AUG-1995: | 95US-0509962. | |
| PR | 08-OCT-1997: | 97US-0947201. | |
| XX | 22-NOV-1994: | 94US-0343380. | |
| XX | | | |
| PA | (NASC-) NAT SCI COUNCIL ROC. | | |
| XX | | | |
| PI | Yu S, Liu L, Chan M; | | |
| XX | | | |
| DR | WPI: 2001-647191/74. | | |
| DR | N-PSDB: AAI70537. | | |
| XX | | | |
| PT | Producing a transgenic monocot plant comprising a transgene under | | |
| PT | control of an alpha amylase promoter and signal peptide sequences, | | |
| PT | provides transgenic plants particularly cereals for the brewing | | |
| XX | | | |
| PS | Example 1; Column 61-64; 44pp; English. | | |
| XX | | | |
| CC | The present sequence is that of rice (<i>Oryza sativa</i>) cv. M202 | | |
| CC | alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C | | |
| CC | (see AAI70537). Expression of alpha-Amy7-C in cultured suspension | | |
| CC | cells of rice was induced 6-fold at day 12 after sugar depletion, | | |
| CC | and continued to increase up to day 14. The invention relates to | | |
| CC | the use of an alpha-amylase gene promoter and signal sequence in | | |
| CC | the production of recombinant proteins in transgenic plants and | | |
| CC | transgenic plant seeds. In a claimed method, a transgenic monocot | | |
| CC | is obtained by: transforming an immature embryo of the plant via | | |
| CC | Agrobacterium-mediated transformation with DNA comprising a plant | | |
| CC | alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that | | |
| CC | is induced under sugar-depleted or sugar-free conditions, a signal | | |
| CC | peptide sequence, and an exogenous sequence encoding a gene product; | | |
| CC | regenerating the transformed plant; and growing the transgenic | | |
| CC | plant, which expresses the gene product under sugar-depleted or | | |
| CC | sugar-free conditions. The gene product may also be obtained by | | |
| CC | cultivating an angiosperm host cell. The transgenic monocot plants | | |
| CC | are especially useful in brewing and to produce glucose from starch. | | |
| XX | | | |
| SO | Sequence 428 AA; | | |
| | | | |
| Query Match | 68.0%; Score 41.5; DB 22; Length 428; | | |
| Best Local Similarity | 80.0%; Pred. No. 48; | | |
| Matches | 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1; | | |
| QY | 1 CRDDRPYADG 10 | | |
| | | | |
| Db | 149 CRDD-PYGDG 157 | | |
| | | | |
| RESULT 6 | | | |
| AAID | AAAB97245 | | |
| XX | AAAB97245 standard; Protein: 428 AA. | | |
| CC | AAAB97245; | | |
| XX | | | |
| DT | 31-JUL-2001 (first entry) | | |
| XX | | | |
| DE | Alpha-amylase related protein #1. | | |
| XX | | | |
| KW | Alpha-amylase; promoter; expression vector; rice. | | |
| XX | | | |
| OS | Unidentified. | | |
| XX | | | |
| PN | TW402638-A. | | |
| XX | | | |
| PD | 21-AUG-2000. | | |
| XX | | | |
| PF | 13-FEB-1992; 97TW-0101436. | | |
| XX | | | |
| PR | 13-FEB-1992; 97TW-0101436. | | |
| XX | | | |
| PA | (NASC-) NAT SCI COUNCIL. | | |

| | |
|-------------------------|---|
| XX | Yu S, Liou L; |
| PI | WPI: 2001-167365/17. |
| DR | N-PSDB: AAH20283. |
| XX | |
| PT | Gene expression system comprising the promoter region of alpha-amylase |
| PT | gene, produces large quantities of alpha-amylase in culture medium of |
| PT | sugar starved rice - |
| XX | |
| PS | Disclosure: Fig 8; 104pp; Chinese. |
| XX | |
| CC | This invention relates to a gene expression system comprising the |
| CC | alpha-amylase gene promoter. DNA encoding the signal peptide of |
| CC | alpha-amylase and the promoter along with the glucuronidase reporter gene |
| CC | and hygromycin resistance gene are used in the construction of a GUS gene |
| CC | expression vector, which when transformed into rice suspension-cultured |
| CC | cells, can be used to investigate the expression of the vector under the |
| CC | control of the promoter. The gene expression system can be used to |
| CC | conduct gene regulation and protein expression and secretion using the |
| CC | characteristics of the alpha-amylase gene promoter and the DNA sequence |
| CC | encoding the signal peptide. The present sequence represents an |
| CC | alpha-amylase related protein used in the course of the present |
| CC | invention. |
| XX | |
| XX | Sequence 428 AA; |
| XX | |
| Query Match | 68.0%; Score 41.5; DB 22; Length 428; |
| Best Local Similarity | 80.0%; Pred. No. 48; |
| Matches 8; Conservative | 0; Mismatches 1; Indels 1; Gaps 1; |
| OY | 1 CRDDRPYADG 10 1111 |
| Db | 149 CRDD-PYGDG 157 |
| XX | |
| RESULT 7 | |
| ID | AA076520 standard; Protein: 429 AA. |
| XX | |
| AC | AA076520; |
| XX | |
| DT | 14-FEB-1996 (first entry) |
| XX | |
| DE | Alpha-amylase-7-C. |
| XX | |
| KW | Alpha-Amy-6-C; amylase; promoter; vector; heterologous; |
| KW | gene expression system. |
| XX | |
| OS | Oryzae sativa. |
| XX | |
| XX | |
| Key | Location/Qualifiers |
| FT | Misc-difference 35 |
| FT | /note= "corresp. to GAC codon" |
| FT | Misc-difference 83 |
| FT | /note= "corresp. to CAG codon" |
| FT | Misc-difference 158 |
| FT | /note= "corresp. to GAC codon" |
| FT | Misc-difference 218 |
| FT | /note= "corresp. to TAC codon" |
| FT | Misc-difference 224 |
| FT | /note= "corresp. to CGG codn" |
| FT | Misc-difference 233 |
| FT | /note= "corresp. to CGT codon" |
| FT | Misc-difference 294 |
| FT | /note= "corresp. to CAG codon" |
| XX | |
| PN | JP07143895-A. |
| XX | |
| DD | 06-JUN-1995. |
| XX | |
| FP | 04-NOV-1993; 93JP-0297607. |
| XX | |

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PR 05-NOV-1992; 92JP-0321274.
XX
XX (MASC-) NAT SCI COUNCIL.
XX
XX WPI; 1995-236472/31.
DR N-PSDB; AAQ92806.
XX
XX Gene expression system contg. alpha-amylase gene promoter - for use
XX in plants for expression of heterologous genes
XX
XX Claim 3; Page 27-30; 42pp; Japanese.
XX
XX AAAR6519-R75521 represent the amylase gene products alpha-amylase-6-C,
XX alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter
XX regions of these amylase genes are used in a new gene expression system.
XX The system may be used for the expression of heterologous genes in plant
XX cells and for the large scale production of the encoded products of such
XX genes.
XX NB. Some amino acids in this sequence appear to have been wrongly
XX entered, see feature table and the corresp. DNA file AAQ92806.
SQ
XX
XX Sequence 429 AA:
XX
XX Query Match 68.0%; Score 41.5; DB 16; Length 429;
XX Best Local Similarity 80.0%; Pred. No. 48;
XX Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX 1 CRDDRPYADG 10
XX |||| || ||
DB 150 CRDD-PYGDG 158
XX
XX
XX RESULT 8
XX AAAR55130 standard; Protein; 433 AA.
XX
XX AAAR55130;
XX
XX 25-MAR-2003 (updated)
XX 12-JAN-1995 (first entry)
XX
XX Rice alpha-amylase coding.
XX
XX Virus; recombinant; plant virus; alpha trichosanthin; phenotype;
XX alpha amylase; alpha hemoglobin; bromo mosaic virus; gemini virus;
XX rice necrosis virus tobamovirus; gene expression; chinese cucumber.
XX
XX Oryza sativa.
XX
XX US5316931-A.
XX
XX 31-MAY-1994.
XX
XX 31-JUL-1992; 92US-0923692.
XX
XX 26-FEB-1988; 88US-0160766.
XX 26-FEB-1988; 88US-0160771.
XX 15-JUL-1988; 88US-0219279.
XX 17-FEB-1989; 89US-0310881.
XX 05-MAY-1989; 89US-0347637.
XX 08-JUN-1989; 89US-0363138.
XX 22-OCT-1990; 90US-0600244.
XX 16-JAN-1991; 91US-0641617.
XX 26-JUL-1991; 91US-0737899.
XX 01-AUG-1991; 91US-0739143.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX
XX Dawson WO, Donson J, Garger SJ, Grantham GL, Gr111 LK;
XX Turpen AM, Turpen TH;
XX
XX WPI; 1994-176269/21.
XX
XX N-PSDB; AAQ65574.

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XX
XX New recombinant plant viral nucleic acid - capable of systemic
XX infection and stable expression of non-native nucleic acid in
XX plant host
XX
XX Example 4; Columns 53-56; 44pp; English.
XX
XX The rice alpha-amylase gene may be inserted into a recombinant plant
XX virus which can then be used to infect plants for the production of
XX non-native products (in this case alpha-amylase). Other genes which
XX may be inserted into the virus are those which control a phenotypic
XX trait, such as male sterility, or sequences encoding anti-sense RNA
XX which can be useful to prevent the expression of undesired phenotypic
XX traits. The recombinant virus is derived from a plus sense, single
XX stranded virus selected from tobamovirus, bromo mosaic virus, rice
XX necrosis virus or a gemini virus.
XX (updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 433 AA:
XX
XX Query Match 68.0%; Score 41.5; DB 15; Length 433.
XX Best Local Similarity 80.0%; Pred. No. 49;
XX Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX 1 CRDDRPYADG 10
XX |||| || ||
DB 154 CRDD-PYGDG 162
XX
XX
XX RESULT 9
XX AAR32987 standard; Protein; 434 AA.
XX
XX AAR32987;
XX
XX 25-MAR-2003 (updated)
XX 17-JUN-1993 (first entry)
XX
XX Rice alpha-amylase.
XX
XX Recombinant products; commercial production; fermentation;
XX biosynthesis; natural products; recombinant proteins;
XX product expression; protein expression; expressed proteins.
XX
XX Oryza sativa.
XX
XX WO9303161-A1.
XX
XX 18-FEB-1993.
XX
XX 31-JUL-1992; 92WO-US06359.
XX
XX 01-AUG-1991; 91US-0739143.
XX
XX (DAMS/) DAWSON W O.
XX (DONS/) DONSON J.
XX (GARG/) GARGER S J.
XX (GRAN/) GRANTHAM G L.
XX (GRIL/) GRILLE L K.
XX (TURP/) TURPEN A M.
XX (TURP/) TURPEN T H.
XX
XX Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM, Garger SJ;
XX Grille LK;
XX
XX WPI; 1993-076518/09.
XX
XX N-PSDB; AAQ37680.
XX
XX Recombinant plant viral nucleic acids - used to express a prod.,
XX e.g. antibody or IL-1 in a plant
XX
XX Example 4; Page 96; 30pp; English.
XX

```


PS Example 4; Columns 47-51; 46pp; English.

XX The invention relates to a recombinant plant viral nucleic acid derived
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
 CC that is native to the plus sense, single stranded RNA plant virus and
 CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (1) (a) and
 CC (b) are incapable of recombination with one another, (11) either the
 CC first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic and
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 20; Length 434;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRPADG 10
 |||||
 DB 155 CRDD-PYGDG 163

RESULT 12

AAW84383
 ID AAW84383 standard; Protein: 434 AA.
 XX
 AC AAW84383;
 XX
 DT 01-APR-1999 (first entry)
 XX
 DE Rice alpha-amylase sequence.
 XX
 KM Rice, alpha-amylase; plant virus; RNA plant virus promoter;
 KM systemic infection; foreign gene expression; AIDS therapeutic drug.
 XX
 OS Oryza sativa.
 XX
 PN US5866785-A.
 XX
 PD 02-FEB-1999.
 XX
 PF 07-JUN-1995; 95US-0482920.
 XX
 PR 31-JUL-1992; 92US-0923692.
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 17-FEB-1988; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 PR 19-JUN-1994; 94US-0184237.
 PR 07-JUN-1995; 95US-0482920.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX WPI: 1999-142035/12.

DR N-PSDB; AAX03386.

XX Recombinant plant viral vector - that is capable of systemic
 PT infection in host plant and stable production of heterologous DNA
 PT useful for producing therapeutic proteins for treating e.g. AIDS
 XX
 PS Example 4; Columns 51-54; 45pp; English.

XX The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the
 CC invention. The specification describes a recombinant plant viral
 CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
 CC a native (+)-sense RNA plant virus promoter that is linked to an
 CC expression sequence and a heterologous (+)-sense RNA plant virus
 CC promoter that is linked to an expression sequence. The promoters are
 CC incapable of recombination with each other, and one of the expression
 CC sequences encodes a plant viral coat protein while the other is
 CC optionally a heterologous coding sequence. The plant viral nucleic acid
 CC is capable of systemic infection in a host plant. The viral construct is
 CC useful for the introduction and expression of non-viral foreign genes
 CC in plants and the production of e.g. potential AIDS therapeutic drugs.
 CC
 SQ Sequence 434 AA;

Query Match 68.0%; Score 41.5; DB 20; Length 434;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRPADG 10
 |||||
 DB 155 CRDD-PYGDG 163

RESULT 13

AAW87792
 ID AAW87792 standard; Protein: 434 AA.
 XX
 AC AAW87792;
 XX
 DT 24-AUG-2000 (first entry)
 XX
 DE Rice alpha-amylase protein.
 XX
 KM Animal RNA virus; viral coat protein; plant; male sterility;
 KM Interleukin; EPO; erythropoietin; CSF; colony stimulating factor;
 KM Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;
 KM stereo specific catalysts; alpha-amylase; rice.
 XX
 OS Oryza sativa.
 XX
 PN US6054566-A.
 XX
 PD 25-APR-2000.
 XX
 PF 07-JUN-1995; 95US-0484341.
 XX
 PR 17-FEB-1989; 89US-0310881.
 PR 08-JUN-1989; 89US-0363138.
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 89US-0219279.
 PR 05-MAY-1989; 89US-0347637.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 PR 31-JUL-1992; 92US-0923692.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO, Turpen AM;
 PI Donson J;
 XX

DR WPI: 2000-338510/29.
 DR N-PSDB; AAA12394.
 XX
 PT Recombinant non-retroviral nucleic acid for producing proteins such as
 PT interleukin, melanin and vaccines, comprises subgenomic promoters
 PT linked to sequences coding for viral coat protein and heterologous
 PT proteins -
 XX
 PS Example 4; Column 65-68; 51pp; English.
 XX
 CC This invention describes a novel recombinant viral nucleic acid (1)
 CC from a non-retroviral (+) sense, single stranded animal RNA virus
 CC comprising a nucleic acid sequence coding for a viral coat protein
 CC regulated by a native subgenomic promoter and other two heterologous
 CC nucleic acid sequences regulated by two other subgenomic promoters.
 CC (1) is useful for expressing foreign genes e.g. genes inducing male
 CC sterility in plants. (1) is also useful for producing proteins such as
 CC interleukin, EPO (erythropoietin), CSF (colony stimulating factor),
 CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
 CC etc., and enzymes that are useful for stereo specific catalysis of
 CC organic compounds. (1) is stable and transcribed systemically. The dual
 CC subgenomic promoter system reduces the frequency of recombination thus
 CC reducing regeneration of the wild type virus. This sequence represents
 CC a rice alpha-amylase protein which is described in the method of the
 CC invention.
 CC
 AC Sequence 434 AA;
 SQ
 Query Match 68.0%; Score 41.5; DB 21; Length 434;
 Best Local Similarity 80.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 CRDDRPYADG 10
 11111111
 Db 155 CRDD-PYGDG 163
 11111111
 RESULT 14
 AAR07669
 ID AAR07669 standard; protein; 215 AA.
 AC AAR07669;
 XX
 XX 25-MAR-2003 (updated)
 DT 15-FEB-1991 (first entry)
 DE Partial alpha-amylase precursor coded by clone Amyz6 from potato.
 XX
 KW potato; alpha-amylase; starch degradation.
 XX
 OS Solanum tuberosum.
 XX
 PN WO9012876-A.
 XX
 PD 01-NOV-1990.
 XX
 XX 24-APR-1990; 90WO-DK00108.
 PF
 XX 24-APR-1989; 89DK-0001980.
 PR
 XX (DASP-) DANSKE SPRITFABRIKKER DANISCO AS.
 PA (DANI-) DANISCO A/S.
 XX
 PI Gausing K, Kreiberg JD;
 XX
 DR WPI: 1990-348479/46.
 DR N-PSDB; AAQ06479.
 XX
 PT DNA fragments encoding alpha-amylase in dicotyledonous plants -
 PT are used for detecting gene organisation etc.
 XX
 PS Claim 26; Fig 4; 1pp; English.
 XX

CC Amyz6 was isolated from a cDNA library prepared from RNA
 CC extracted from sprouts of a potato. The library was screened with a
 CC barley alpha amylase probe. The nucleic acid sequence encodes a
 CC partial alpha-amylase precursor commencing at amino acid residue
 CC 133 of the full-length protein.
 CC See also AA006476-8 and AAQ06553.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC
 AC Sequence 215 AA;
 SQ
 Query Match 67.2%; Score 41; DB 11; Length 215;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 11111111
 Db 5 CRDDPYSDG 14
 11111111
 RESULT 15
 ABB59190
 ID ABB59190 standard; Protein; 594 AA.
 AC ABB59190;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 4362.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KM
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL03293.
 DR
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX Disclosure; SEQ ID NO 4362; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 AC Sequence 594 AA;
 SQ
 Query Match 63.9%; Score 39; DB 22; Length 594;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRYPAD 9
 1:|||||
 DB 463 CKDRAYED 471

RESULT 16

AA050253
 ID AAM50253 standard; Protein; 435 AA.

AC AAM50253;

DT 21-JAN-2002 (first entry)

DE Rice alpha-amylase (alpha-Amy3-C gene product).

KM Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
 KW monocot; cereal; brewing.

OS Oryza sativa.

FI Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT /label= Mature_protein

PN US6288302-B1.

PD 11-SEP-2001.

PF 04-MAY-1998; 98US-0072917.

PR 04-NOV-1992; 92US-0973324.

PR 01-AUG-1995; 95US-0509662.

PR 08-OCT-1997; 97US-0947201.

PR 22-NOV-1994; 94US-0343380.

PA (NASC-) NAT SCI COUNCIL ROC.

PI Yu S, Liu L, Chan M.

DR WPI: 2001-647191/74.

DR N-PSDB; AAI70540.

PT Producing a transgenic monocot plant comprising a transgene under
 PT control of an alpha amylase promoter and signal peptide sequences,
 PT provides transgenic plants particularly cereals for the brewing
 PT industry -

PS Disclosure: Column 79-82; 44pp; English.

CC The present sequence is that of alpha-amylase encoded by DNA clone
 CC alpha-Amy3-C (see AAI70540). Expression of alpha-Amy3-C increases
 CC 5-fold following sugar starvation. The invention relates to
 CC the use of an alpha-amylase gene promoter and signal sequence in
 CC the production of recombinant proteins in transgenic plants and
 CC transgenic plant seeds. In a claimed method, a transgenic monocot
 CC is obtained by: transforming an immature embryo of the plant via
 CC Agrobacterium-mediated transformation with DNA comprising a plant
 CC alpha-amylase promoter (e.g. the rice alpha-Amy3-C promoter) that
 CC is induced under sugar-depleted or sugar-free conditions, a signal
 CC peptide sequence, and an exogenous sequence encoding a gene product;
 CC regenerating the transformed plant; and growing the transgenic
 CC plant, which expresses the gene product under sugar-depleted or
 CC sugar-free conditions. The gene product may also be obtained by
 CC cultivating an angiosperm host cell. The transgenic monocot plants
 CC are especially useful in brewing and to produce glucose from starch.

SO Sequence 435 AA;
 Query Match 62.3%; Score 38; DB 22; Length 435;
 Best Local Similarity 60.0%; Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CRDDRYPADG 10
 1:|||||
 DB 148 CSDDTYSDG 157

RESULT 17

AA097247
 ID AAB97247 standard; Protein; 435 AA.

AC AAB97247;

DT 31-JUL-2001 (first entry)

DE Alpha-amylase related protein #3.

KW Alpha-amylase; promoter; expression vector; rice.

OS unidentified.

PN TW402638-A.

PD 21-AUG-2000.

PF 13-FEB-1992; 97TW-0101436.

PR 13-FEB-1992; 97TW-0101436.

PA (NASC-) NAT SCI COUNCIL.

PI Yu S, Liu L;

DR WPI: 2001-167365/17.

DR N-PSDB; AAH20285.

PT Gene expression system comprising the promoter region of alpha-amylase
 PT gene, produces large quantities of alpha-amylase in culture medium of
 PT sugar starved rice -

PS Disclosure: Fig 12; 104pp; Chinese.

CC This invention relates to a gene expression system comprising the
 CC alpha-amylase gene promoter. DNA encoding the signal peptide of
 CC alpha-amylase and the promoter along with the glucuronidase reporter gene
 CC and hygromycin resistance gene are used in the construction of a GUS gene
 CC expression vector, which when transformed into rice suspension-cultured
 CC cells, can be used to investigate the expression of the vector under the
 CC control of the promoter. The gene expression system can be used to
 CC conduct gene regulation and protein expression and secretion using the
 CC characteristics of the alpha-amylase gene promoter and the DNA sequence
 CC encoding the signal peptide. The present sequence represents an
 CC alpha-amylase related protein used in the course of the present
 CC invention.

SO Sequence 435 AA;

Query Match 62.3%; Score 38; DB 22; Length 435;
 Best Local Similarity 60.0%; Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRYPADG 10
 1:|||||
 DB 148 CSDDTYSDG 157

RESULT 18

AA081063
 ID AAB81063 standard; Protein; 1036 AA.

AC AAB81063;

DT 02-JUN-1999 (first entry)

```

XX XX Amino acid sequence of the Drosophila smoothened polypeptide.
DE XX
XX XX Drosophila: smoothened gene; smoothened peptide; SP;
KW cell proliferation; cell differentiation; spermatogenesis;
KW osteogenesis; chondrogenesis; apoptosis; degenerative disorder;
KW neoplastic disorder; hyperplastic disorder; varicella-zoster;
KW tumour; liver repair.
XX XX
XX OS Drosophila sp.
XX PN MO9901468-A2.
XX PD 14-JAN-1999.
XX PF 01-JUL-1998; 98WO-US13793.
XX PR 21-JUL-1997; 97US-0897798.
XX PR 01-JUL-1997; 97US-0051407.
XX XX
XX PA (INGH/) INGHAM P W.
XX PA (ONTO-) ONTOGENY INC.
XX PA (VHEU/) VAN DEN HEUVEL M.
XX DR WPI: 1999-105996/09.
XX DR N-PSDB; AAV99968.
XX XX
XX PT New isolated smoothened genes - used to develop products for
XX PT treating e.g. cancers, neurodegenerative disorders, nervous system
XX PT injury, immunological diseases or infections
XX PS Claim 1; Pages 94-97; 107pp; English.
XX XX
XX CC This is the amino acid sequence of the novel Drosophila smoothened
XX CC polypeptide (SP) used in the method of the invention. The SPs can
XX CC modulate at least one of proliferation, differentiation or survival
XX CC of a cell which expresses the SP. The products can be used to
XX CC modulate spermatogenesis, osteogenesis, chondrogenesis or neuronal
XX CC cell differentiation or to enhance survival of neuronal cells, e.g.
XX CC to prevent apoptosis. They can be used for treating e.g.
XX CC degenerative disorders marked by loss of particular cell-types,
XX CC apoptosis, neoplastic and/or hyperplastic disorders. In particular
XX CC they can be used to treat neurological conditions derived from
XX CC acute, subacute, or chronic injury to the nervous system, aging of
XX CC the nervous system, chronic neurodegenerative diseases of the
XX CC nervous system, chronic immunological diseases of the nervous
XX CC system or affecting the nervous system. They can also treat be used
XX CC to CNS trauma infarction, infection (such as viral infection with
XX CC varicella-zoster), metabolic disease, nutritional deficiency,
XX CC toxic agents (such as cisplatin treatment), chronic pain syndromes
XX CC or in nerve prostheses for the repair of central and peripheral
XX CC nerve damage, malignant gliomas, medulloblastomas, neuroectodermal
XX CC tumours, ependymomas and for liver repair and regeneration of lung
XX CC tissue in the treatment of emphysema, or for enhancing bond
XX CC formation, tissue formation or fertility. The products can also be
XX CC used for detection, diagnosis and drug screening.
XX SQ Sequence 1036 AA;

Query Match 62.3%; Score 38; DB 20; Length 1036;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 RDDRPYADG 10
DB 68 RDDKPFWDG 76

```

```

XX XX 26-MAR-2002 (first entry)
DE XX
XX XX Drosophila melanogaster polypeptide SEQ ID NO 4761.
DE XX
XX XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX XX
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX XX
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PMD, Myers EW;
XX DR WPI: 2001-656860/75.
XX DR N-PSDB; ABL03426.
XX XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 4761; 21pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1036 AA;

Query Match 62.3%; Score 38; DB 22; Length 1036;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 RDDRPYADG 10
DB 68 RDDKPFWDG 76

RESULT 20
AAB28647
ID AAB28647 standard; Protein; 1036 AA.
XX AC AAB28647;
XX DT 13-FEB-2001 (first entry)
XX DE Drosophila smoothened.
XX DE Drosophila: smoothened; cell proliferation; cell differentiation;
KW cell signalling.
XX OS Drosophila melanogaster.
XX PN US6136958-A.
XX PD 24-OCT-2000.

```

```

XX 30-SEP-1997; 97US-0953823.
PF
XX
PR 30-SEP-1996; 96US-0027070.
XX
PA (GETH ) GENENTECH INC.
XX
XX Stone DM, De Sauvage FJ, Rosenthal A;
XX
DR WPI: 2001-006229/01.
XX
PT Antibodies to vertebrate smoothened proteins which relate to Hedgehog
PT and patched signaling molecules involved in cell proliferation and
PT differentiation
XX
PS Example 3; Fig 5; 38pp; English.
XX
CC The present sequence was used for comparison studies with vertebrate
CC smoothened polypeptides. Smoothened interacts with Hedgehog and Patched
CC signalling molecules involved in cell proliferation and differentiation.
CC Rat smoothened cDNA was isolated from an embryonic day 9-10 rat cDNA
CC library. The rat smoothened cDNA was then used as a probe to isolate the
CC human homologue from a human embryonic lung cDNA library. Antibodies
CC which specifically bind to the vertebrate smoothened polypeptides were
CC identified.
XX
SQ Sequence 1036 AA;
Query Match 62.3%; Score 38; DB 22; Length 1036;
Best Local Similarity 66.7%; Pred. No. 4,9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 CRDPRPYADG 10
DB 68 RDXKPFWDG 76

RESULT 21
AAR07159
ID AAR07159 standard; protein; 17 AA.
XX
AC AAR07159;
XX
XX 24-JAN-1991 (first entry)
XX
XX Synthetic Nerve growth factor (NGF) peptide fragment.
XX
XX Nervous disorders; Alzheimer's disease; Parkinson's disease; stroke.
XX
XX Synthetic.
XX
XX WO9010644-A.
XX
XX 20-SEP-1990.
XX
XX 08-MAR-1990; 90MO-0000149.
XX
XX 14-MAR-1989; 89SE-0000899.
XX
XX (LOPE-) LOPE MED AB.
XX
XX Olson L, Persson H, Ebendal T;
XX
XX WPI: 1990-304983/40.
XX
XX
XX New peptide fragments of nerve growth factor or its precursor -
XX used to raise specific antibodies for immunoassay, esp. for brain
XX tissue
XX
XX Disclosure; Page 11; 24pp; English.
XX
XX Peptides are Abs raised to them are useful in detecting the presence
XX of NGF and precursors, allowing early diagnosis and treatment of
CC

```

```

CC nervous disorders eg. Alzheimer's and Parkinson's disease, spinal
CC cord injury, stroke etc.
CC Peptide corresponds to AAs 54 to 69 of chicken NGF.
XX
XX
SQ Sequence 17 AA;
Query Match 60.7%; Score 37; DB 11; Length 17;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CRDPRPYADG 10
DB 5 CRDPRPVSSG 14

RESULT 22
AAR29474
ID AAR29474 standard; Protein; 42 AA.
XX
AC AAR29474;
XX
XX 25-MAR-2003 (updated)
XX
XX 22-APR-1993 (first entry)
XX
XX NGF, chicken.
XX
XX Neurotrophin; NT; nerve growth factor; NGF;
XX brain-derived neurotrophic factor; BDNF; probe; primer.
XX
XX Gallus sp.
XX
XX WO9220365-A1.
XX
XX 26-NOV-1992.
XX
XX 20-MAY-1992; 92MO-US04266.
XX
XX 21-MAY-1991; 91US-0703450.
XX
XX 12-JUL-1991; 91US-0729253.
XX
XX 23-JUL-1991; 91US-0734422.
XX
XX 28-AUG-1991; 91US-0751356.
XX
XX 20-SEP-1991; 91US-0762674.
XX
XX 14-NOV-1991; 91US-0791924.
XX
XX (REG-) REGENERON PHARM INC.
XX
XX Hallbook F, Ibanez Moliner CF, Persson HB, Yancopoulos GD;
XX
XX WPI: 1992-415468/50.
XX
XX N-PSDB; AAQ32200.
XX
XX Use of neurotrophin-4 for promoting growth and survival of nerve
XX cells - useful in treating neurological, fertility and
XX immunological disorders and in diagnosis
XX
XX Disclosure; Page 96-97; 180pp; English.
XX
XX Oligonucleotide probes and primers were synthesised based on the NT
XX family including NGF, BDNF and NT-3. These were used to isolate DNA
XX encoding NT-4 from nucleic acid from Xenopus ovaries. This DNA was
XX then used to isolate other mammalian DNA encoding NT-4, including
XX human NT-4 DNA.
XX
XX (updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 42 AA;
Query Match 60.7%; Score 37; DB 13; Length 42;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 CRDPRPYADG 10
DB 2 CRDPRPVSSG 11

```

```

RESULT 23
AAR41885
ID AAR41885 standard; peptide; 56 AA.
XX
XX
AC AAR41885;
XX
XX 25-MAR-2003 (updated)
DT 22-APR-1994 (first entry)
XX
DE Granulin E.
XX
XX Granulin; keratinocytes; wound healing; inhibition; peptide;
KM granulocytes; leucocytes.
OS
XX Homo sapiens.
XX
XX W09315195-A1.
XX
XX 05-AUG-1993.
XX
XX 28-FEB-1992; 92MO-CA00089.
XX
XX 03-FEB-1992; 92US-0829233.
XX
XX (SOLO/) SOLOMON S.
XX
XX Solomon S;
XX
XX WPI. 1993-320328/40.
XX
XX New cystine rich granulin peptide(s) from leucocyte(s) - are
PT keratinocyte inhibitors useful topically for wound healing
PS Claim 8; Page 33; 53pp; English.
XX
XX The granulin inhibits keratinocytes and is useful in formulations
CC for promoting the healing of wounds. This peptide was designated
CC granulin E.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 56 AA:
SQ
Query Match 60.7%; Score 37; DB 14; Length 56;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
QY 1 CRDDR-----PYADG 10
DB 17 CRDREGWACCPYAGG 32

```

```

PD 05-DEC-2002.
XX
XX 24-MAY-2002; 2002MO-US16540.
XX
XX 25-MAY-2001; 2001US-293823P.
XX 13-JUL-2001; 2001US-305510P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Hempstead BL, Lee R, Teng KK, Kermani P;
XX
XX WPI. 2003-140406/13.
XX
XX Novel protein for inducing apoptosis, has proneurotrophin pro-domain
PT with conserved regions, mature neurotrophin domain, and connector that
PT joins conserved region to mature domain and resistant to protease
PT cleavage -
XX
XX Disclosure; Page 23; 124pp; English.
XX
XX The invention relates to an isolated protein comprising a pro-domain (PD)
CC of a proneurotrophin, where PD comprises a pro-domain conserved region,
CC or a modified proneurotrophin protein (Ib) with a PD, a mature
CC neurotrophin domain (MD), and a connector that joins the pro-domain
CC conserved region to MD and resistant to protease cleavage. The PD is
CC selected from specific peptide fragments of human nerve growth factor
CC (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin
CC 3 (NT-3) or human neurotrophin 4/5 (NT4/5). (Ib) is useful for inducing
CC apoptosis in a cell comprising p75 receptors (normal number or higher
CC than the normal number of p75 receptors) on its surface, by causing the
CC p75 receptor to bind (Ib), in vitro, in mammals or humans. The method is
CC useful for treating vascular smooth muscle plaque e.g. atherosclerotic
CC plaque. The cell is a malignant cell e.g. cells of tumour, melanoma,
CC prostate, pancreas, nervous system (e.g. medulloblastoma or astrocytoma),
CC leukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte,
CC heart, vascular smooth muscle or neural cell. A molecule that inhibits
CC the binding of proneurotrophin to a p75 receptor is useful in a method
CC for inhibiting apoptosis of a cell in a mammal e.g. human suffering from
CC a condition associated with undesired apoptosis due to binding of a
CC proneurotrophin to p75 receptor. The condition is the result of an injury
CC or an environmental insult, e.g. nervous system injury, caused by a
CC chemical or radiation or occurring during cancer treatment, hypoxic
CC ischaemia caused by stroke or heart attack, viral or microbial infection,
CC meningitis, encephalitis or abscesses, neurodegenerative disorders e.g.
CC Alzheimer's disease, familial dysautonomia, ataxia telangiectasia,
CC Charcot-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular
CC atrophy or Friedreich's ataxia, or multiple sclerosis, convulsions,
CC epilepsy and spinal cord injury. Sequences ABB71151-60 represent pro and
CC mature domains of NGF from various species.
XX
XX Sequence 118 AA:
SQ
Query Match 60.7%; Score 37; DB 24; Length 118;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CRDDRPYADG 10
DB 57 CRDPRPVSSG 66

```

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RESULT 25
ABR41533
ID ABR41533 standard; protein; 346 AA.
XX
XX ABR41533;
XX
XX 02-JUN-2003 (first entry)
XX
XX Human DTHP protein modification/maintenance protein.
XX
XX Human; dthp; diagnostic and therapeutic polynucleotide; diagnosis;
XX cancer; cell proliferative disorder; autoimmune disorder;
XX
XX

```

inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 inflammatory disorder; gastrointestinal disorder; transpotic disorder;
 neurological disorder; gastrointestinal disorder; transpotic disorder;
 connective tissue disorder; drug screening; proteome analysis;
 gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 disease model; toxicological testing; transcript imaging;
 protein modification; protein maintenance.
 Homo sapiens.
 WO200297031-A2.
 05-DEC-2002.
 27-MAR-2002; 2002WO-US10056.
 28-MAR-2001; 2001US-279619P.
 29-MAR-2001; 2001US-280067P.
 29-MAR-2001; 2001US-280068P.
 15-MAY-2001; 2001US-281280P.
 17-MAY-2001; 2001US-281829P.
 17-MAY-2001; 2001US-281849P.
 19-JUN-2001; 2001US-289428P.
 20-JUN-2001; 2001US-289776P.
 20-JUN-2001; 2001US-300001P.
 (INCYTE GENOMICS INC.
 Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;
 Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
 WPI: 2003-129518/12.
 N-PSDB: ACC46471.
 Novel human diagnostic and therapeutic polypeptide useful for
 identifying test compound which specifically binds to a polypeptide
 encoded by human diagnostic and therapeutic polynucleotide, and to
 induce antibodies
 Claim 27; SEQ ID No 1068; 591pp; English.
 The invention relates to novel human diagnostic and therapeutic
 polynucleotides designated dithp (ACC46080-ACC46749) and to their
 encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 to polynucleotide sequences at least 90% identical to the dithp cDNA
 sequences of the invention; recombinant vectors, host cells and
 transgenic organisms comprising a dithp nucleic acid sequence; the
 recombinant production of DITHP proteins; antibodies specific for DITHP
 proteins; microarrays comprising dithp nucleic acid sequences; methods
 of detecting dithp nucleotide and protein sequences; methods of screening
 for compounds which specifically bind a DITHP protein; and methods of
 assessing the toxicity of test compounds using a dithp hybridisation
 probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 diagnosis of a wide variety of conditions including cancer and other cell
 proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 viral, fungal or parasitic infections; hormonal disorders; metabolic
 disorders; neurological disorders; gastrointestinal disorders; transport
 disorders; and connective tissue disorders. They may also be used to
 screen for modulators of protein activity or gene expression. DITHP
 proteins can additionally be used in analysis of the proteome of a tissue
 or cell type and to induce antibodies. The dithp nucleic acids are
 additionally useful in somatic or germline gene therapy of the disorders
 mentioned above, as a source of antisense sequences, as a source of
 probes and primers, in genotyping and identification of individuals, in
 the generation of transgenic animal models of human disease or knock in
 humanised animals, in toxicological testing, and in transcript imaging.
 The present sequence represents a DITHP protein which is involved in
 protein modification and/or maintenance.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at http://wipo.int/pub/published_pcc/sequences.

XX Sequence 346 AA.
 SQ Query Match 60.7%; Score 37; DB 24; Length 346;
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CRDREYA 8
 |||::|:|
 DB 244 CRDREYA 251
 RESULT 26
 ABG96343
 ID ABG96343 standard; Protein: 413 AA.
 AC ABG96343;
 DT 11-DEC-2002 (first entry)
 XX Human ovarian cancer marker OV27.
 DE Human ovarian cancer marker OV27.
 XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW non-tuberculous granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker.
 XX Homo sapiens.
 OS
 XX
 PN WO200271928-A2.
 XX 19-SEP-2002.
 PD 14-MAR-2002; 2002WO-US07826.
 PF 14-MAR-2001; 2001US-276025P.
 PR 14-MAR-2001; 2001US-276026P.
 PR 10-AUG-2001; 2001US-311732P.
 PR 19-SEP-2001; 2001US-323580P.
 PR 26-SEP-2001; 2001US-324967P.
 PR 26-SEP-2001; 2001US-325102P.
 PR 26-SEP-2001; 2001US-325149P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleby PO, Mills GB;
 PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatk K;
 XX WPI: 2002-723277/78.
 DR N-PSDB: ABS76439.
 XX Assessing whether a patient is afflicted with ovarian cancer, useful in
 PT assessing the stage or progression of the disease, comprises comparing
 PT the expression level of a cancer marker in a sample from a patient and
 PT from a non cancer patient -
 XX
 PS Disclosure: Page 258-259; 481pp; English.
 XX The present invention relates to a new method for assessing whether a
 CC patient is afflicted with ovarian cancer. The method involves comparing
 CC the expression level of a marker in a patient sample and the normal level
 CC of expression of the marker in a control non-ovarian cancer sample, where
 CC the marker is selected from 363 cancer markers described in the
 CC specification. The method of the invention is useful in diagnosing or
 CC characterising cancer, in detecting the presence of cancer as early as
 CC possible, and the recurrence of ovarian cancer. The method may also be of
 CC particular use with patients having an enhanced risk of developing
 CC ovarian cancer (e.g. patients having a familial history of ovarian
 CC cancer). The cancer markers may be used in the management and treatment

DT 22-APR-1994 (first entry)
XX Granulin sequence.
DE
XX Granulin; keratinocytes; wound healing; inhibition; peptide;
KM granulocytes; leucocytes.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 452
FT /note= "Valine encoded by ATG."
FT Misc-difference 539
FT /note= "Glycine encoded by CAG."
XX
XX MO9315195-A1.
XX
XX PD 05-AUG-1993.
XX
XX PF 28-FEB-1992; 92MO-CA00089.
XX
XX PR 03-FEB-1992; 92US-0829233.
XX
XX (SOLO/) SOLOMON S.
XX
XX Solomon S;
XX
XX WPI: 1993-320328/40.
DR N-PSDB; AAQ49052.
XX
XX New cystine rich granulin peptide(s) from leucocyte(s) - are
PT keratinocyte rich granulin peptides useful topically for wound healing
XX
XX PS Disclosure; Figure 4c; 53pp; English.
XX
XX CC The granulin inhibits keratinocytes and is useful in formulations
CC for promoting the healing of wounds.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 593 AA;
Query Match 60.7%; Score 37; DB 14; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
QY 1 CPDDR-----PYADG 10
DB 534 CRDNRGMAACCPYAG 549
RESULT 29
AAW85475
ID AAW85475 standard; Protein: 593 AA.
XX
XX AAW85475;
XX
DT 15-MAR-1999 (first entry)
XX
XX Human GP88 autocrine growth factor.
XX
XX GP88; granulin; epithelin; human; growth factor; autocrine; tumour;
KM cancer; viral infection; antagonist; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 340..364
FT /note= "E19Y peptide used to raise antibody"
FT 566..579
FT /note= "A14R peptide used to raise antibody"
XX
XX MO9852607-A1.

PD 26-NOV-1998.
XX
XX 22-MAY-1998; 98MO-US10555.
XX
XX 16-DEC-1997; 97US-0991862.
PR 23-MAY-1997; 97US-0863079.
XX
XX (SERR/) SERRERO G.
XX
XX Serrero G;
XX
XX WPI: 1999-045276/04.
DR N-PSDB; AAW82825.
XX
XX Composition containing antagonist of growth factor GP88 - useful for
PT treating cancer and viral diseases and also for diagnosing disease
PT from altered GP88 expression
XX
XX Example 5; Fig 9A; 86pp; English.
XX
XX PS This is the amino acid sequence of human GP88, an 88 kDa
XX glycoprotein autocrine growth factor and epithelin/granulin
CC precursor that is expressed in a tightly regulated manner in normal
CC cells, is overexpressed and upregulated in highly tumorigenic cells
CC derived from normal cells, and which acts as a stringently required
CC growth stimulator for the tumorigenic cells. Inhibition of GP88
CC expression or action in the tumorigenic cells results in an
CC inhibition of the tumorigenic properties of the overproducing
CC cells. Antagonists to GP88 are used to treat diseases associated
CC with increased expression of GP88, particularly cancer but also
CC viral infections. Fragments of GP88 are used to raise specific
CC antibodies (used as antagonists, as diagnostic reagents and for
CC delivering toxins or other compounds to GP88-expressing cells) and
CC to screen for antibodies. Methods are provided for diagnosing
CC disease, or determining susceptibility to disease, resulting from
CC altered GP88 activity.
XX
SQ Sequence 593 AA;
Query Match 60.7%; Score 37; DB 20; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;
QY 1 CPDDR-----PYADG 10
DB 534 CRDNRGMAACCPYAG 549
RESULT 30
AAE20521
ID AAE20521 standard; Protein: 593 AA.
XX
XX AAE20521;
XX
DT 01-JUL-2002 (first entry)
XX
XX Human granulin/epithelin precursor (GP88) protein.
XX
XX Human; granulin precursor; GP88; cytostatic; tumorigenicity; tamoxifen;
KM antineoplastic; antioestrogen therapy; skin cancer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 273
FT /note= "Encoded by AAG"
FT Region 346..364
FT /note= "Region used as antigen to develop anti-human
FT GP88 neutralising antibody"
XX
XX US2002025543-A1.
XX
XX 28-FEB-2002.

XX 15-JUN-2001; 2001US-0880842.

PF

XX

PR 23-MAY-1997; 97US-0863079.

PR

XX

PR 08-DEC-1999; 99US-0456886.

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PA

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Search completed: August 29, 2003, 18:43:59
Job time : 33.5714 secs

Sequence 593 AA:

Query Match 60.7%; Score 37; DB 23; Length 593;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

1 CRDDR-----PYADG 10
|||:| |||
534 CRDNRQGWACCPYAOG 549

Disclosure: Fig 9B; 50pp; English.

The invention relates to a method for diagnosing tumorigenicity in a human. The method comprises obtaining a biological sample containing cells from the patient, detecting GP88 in the cells of the sample, and determining the ratio of GP88 positive cells in the sample, and determining the ratio of GP88 positive cells to the total number of cells in the sample. The invention also relates to a method for determining if a human patient is resistant to the antineoplastic effects of antiestrogen therapy. The method is useful for diagnosing tumorigenicity in a sample, such as blood, serum, plasma, urine, nipple aspirate, cerebrospinal fluid, liver, kidney, breast, bone, brain, lung, colon, or skin cancer. The method can be used to treat or prevent re-occurrence of cancer in a patient, by administering tamoxifen if the sample contains less than 10 % GP88, or less than 5 % GP88 positive cells. The present sequence is human granulocyte/epithelial precursor (GP88) protein.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:38:06 ; Search time 10.5714 Seconds
(without alignments)
40.024 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDDPYADG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents,AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCPMUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|----------------------|
| 1 | 41.5 | 68.0 | 428 | 1 | US-07-973-324A-4 |
| 2 | 41.5 | 68.0 | 428 | 1 | US-08-343-380-4 |
| 3 | 41.5 | 68.0 | 428 | 3 | US-09-072-435-4 |
| 4 | 41.5 | 68.0 | 428 | 3 | US-09-072-917A-4 |
| 5 | 41.5 | 68.0 | 434 | 1 | US-07-923-692C-6 |
| 6 | 41.5 | 68.0 | 434 | 1 | US-08-184-237-6 |
| 7 | 41.5 | 68.0 | 434 | 2 | US-08-482-920-6 |
| 8 | 41.5 | 68.0 | 434 | 3 | US-08-484-341-6 |
| 9 | 41.5 | 68.0 | 434 | 3 | US-08-484-502-6 |
| 10 | 41.5 | 68.0 | 434 | 4 | US-09-726-651A-6 |
| 11 | 38 | 62.3 | 151 | 4 | US-09-252-991A-31890 |
| 12 | 38 | 62.3 | 384 | 4 | US-09-252-991A-24086 |
| 13 | 38 | 62.3 | 435 | 3 | US-09-072-917A-9 |
| 14 | 38 | 62.3 | 500 | 4 | US-09-252-991A-19739 |
| 15 | 38 | 62.3 | 1036 | 2 | US-08-720-484A-5 |
| 16 | 38 | 62.3 | 1036 | 3 | US-08-953-823A-5 |
| 17 | 38 | 62.3 | 1036 | 4 | US-09-398-239-5 |
| 18 | 38 | 62.3 | 1036 | 4 | US-09-560-876A-5 |
| 19 | 38 | 62.3 | 1065 | 4 | US-09-560-876A-6 |
| 20 | 37 | 60.7 | 217 | 4 | US-09-328-352-7068 |
| 21 | 37 | 59.0 | 593 | 4 | US-08-981-862-17 |
| 22 | 36 | 59.0 | 568 | 4 | US-09-252-991A-22461 |
| 23 | 35 | 57.4 | 129 | 4 | US-09-216-393B-62 |
| 24 | 35 | 57.4 | 165 | 3 | US-08-965-689A-6 |
| 25 | 35 | 57.4 | 165 | 3 | US-09-352-967-6 |
| 26 | 35 | 57.4 | 306 | 2 | US-08-484-905-75 |
| 27 | 35 | 57.4 | 306 | 3 | US-08-481-985B-75 |

| | | | | | | |
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| 28 | 35 | 57.4 | 306 | 3 | US-08-370-476-75 | Sequence 75, Appl |
| 29 | 35 | 57.4 | 362 | 2 | US-08-846-762-84 | Sequence 84, Appl |
| 30 | 35 | 57.4 | 444 | 4 | US-09-252-991A-18424 | Sequence 18424, A |
| 31 | 35 | 57.4 | 450 | 4 | US-09-107-532A-4098 | Sequence 4098, A |
| 32 | 35 | 57.4 | 1864 | 2 | US-08-804-227C-3 | Sequence 3, Appl |
| 33 | 34 | 55.7 | 1118 | 4 | US-08-737-109-16 | Sequence 16, Appl |
| 34 | 34 | 55.7 | 277 | 4 | US-09-252-991A-29257 | Sequence 29257, A |
| 35 | 34 | 55.7 | 318 | 4 | US-09-352-991A-31545 | Sequence 31545, A |
| 36 | 34 | 55.7 | 354 | 4 | US-09-252-991A-23146 | Sequence 23146, A |
| 37 | 34 | 55.7 | 475 | 4 | US-09-252-991A-32806 | Sequence 32806, A |
| 38 | 34 | 55.7 | 691 | 4 | US-09-252-991A-16809 | Sequence 16809, A |
| 39 | 34 | 55.7 | 1349 | 4 | US-08-938-291A-6 | Sequence 6, Appl |
| 40 | 34 | 55.7 | 1259 | 4 | US-09-589-619-6 | Sequence 6, Appl |
| 41 | 33 | 54.1 | 437 | 1 | US-09-522-714-18 | Sequence 18, Appl |
| 42 | 33 | 54.1 | 437 | 1 | US-07-973-324A-6 | Sequence 6, Appl |
| 43 | 33 | 54.1 | 437 | 1 | US-08-343-380-6 | Sequence 6, Appl |
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| 46 | 33 | 54.1 | 438 | 1 | US-07-973-324A-2 | Sequence 2, Appl |
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| 48 | 33 | 54.1 | 438 | 3 | US-09-072-435-2 | Sequence 2, Appl |
| 49 | 33 | 54.1 | 438 | 3 | US-09-312-762A-15 | Sequence 15, Appl |
| 50 | 33 | 54.1 | 521 | 4 | US-09-252-991A-18119 | Sequence 18119, A |
| 51 | 33 | 54.1 | 546 | 4 | US-08-311-731A-248 | Sequence 248, App |
| 52 | 33 | 54.1 | 546 | 4 | US-09-252-991A-29573 | Sequence 29573, A |
| 53 | 32.5 | 53.3 | 92 | 4 | US-08-378-548-19 | Sequence 19, Appl |
| 54 | 32 | 52.5 | 139 | 3 | US-08-857-076-20 | Sequence 20, Appl |
| 55 | 32 | 52.5 | 164 | 4 | US-09-252-991A-30657 | Sequence 30657, A |
| 56 | 32 | 52.5 | 202 | 1 | US-08-469-486-56 | Sequence 56, Appl |
| 57 | 32 | 52.5 | 202 | 2 | US-08-469-658-56 | Sequence 56, Appl |
| 58 | 32 | 52.5 | 211 | 4 | US-09-252-991A-26873 | Sequence 26873, A |
| 59 | 32 | 52.5 | 254 | 4 | US-09-252-991A-18250 | Sequence 18250, A |
| 60 | 32 | 52.5 | 314 | 4 | US-09-252-991A-19653 | Sequence 19653, A |
| 61 | 32 | 52.5 | 318 | 4 | US-09-252-991A-22868 | Sequence 22868, A |
| 62 | 32 | 52.5 | 327 | 4 | US-09-252-991A-32140 | Sequence 32142, A |
| 63 | 32 | 52.5 | 327 | 4 | US-09-252-991A-31442 | Sequence 31442, A |
| 64 | 32 | 52.5 | 370 | 4 | US-09-352-991A-26088 | Sequence 26088, A |
| 65 | 32 | 52.5 | 389 | 4 | US-09-134-001C-4316 | Sequence 4316, Ap |
| 66 | 32 | 52.5 | 405 | 4 | US-09-252-991A-24057 | Sequence 24057, A |
| 67 | 32 | 52.5 | 411 | 1 | US-07-602-828A-3 | Sequence 3, Appl |
| 68 | 32 | 52.5 | 411 | 1 | US-07-602-608-2 | Sequence 2, Appl |
| 69 | 32 | 52.5 | 411 | 1 | US-07-983-451-3 | Sequence 3, Appl |
| 70 | 32 | 52.5 | 411 | 1 | US-08-261-578-2 | Sequence 8, Appl |
| 71 | 32 | 52.5 | 411 | 1 | US-08-261-577-8 | Sequence 7, Appl |
| 72 | 32 | 52.5 | 411 | 1 | US-09-070-356-3 | Sequence 3, Appl |
| 73 | 32 | 52.5 | 411 | 3 | US-09-252-991A-27367 | Sequence 27367, A |
| 74 | 32 | 52.5 | 464 | 4 | US-08-489-733-1 | Sequence 1, Appl |
| 75 | 32 | 52.5 | 510 | 1 | US-08-993-581B-1 | Sequence 1, Appl |
| 76 | 32 | 52.5 | 510 | 2 | US-09-134-078-22 | Sequence 22, Appl |
| 77 | 32 | 52.5 | 593 | 1 | US-07-668-648-4 | Sequence 4, Appl |
| 78 | 32 | 52.5 | 593 | 2 | US-08-429-998-4 | Sequence 4, Appl |
| 79 | 32 | 52.5 | 593 | 2 | US-08-431-333-4 | Sequence 4, Appl |
| 80 | 32 | 52.5 | 593 | 2 | PCT-US91-02321-4 | Sequence 4, Appl |
| 81 | 32 | 52.5 | 593 | 4 | US-09-608-790-1 | Sequence 1, Appl |
| 82 | 32 | 52.5 | 616 | 4 | US-09-188-930-303 | Sequence 303, App |
| 83 | 32 | 52.5 | 617 | 3 | US-09-312-283C-303 | Sequence 303, App |
| 84 | 32 | 52.5 | 617 | 4 | US-09-252-991A-31645 | Sequence 31645, A |
| 85 | 32 | 52.5 | 655 | 4 | US-09-252-991A-31565 | Sequence 31565, A |
| 86 | 32 | 52.5 | 833 | 4 | US-09-328-352-4401 | Sequence 4401, Ap |
| 87 | 32 | 52.5 | 944 | 4 | US-09-252-991A-18729 | Sequence 18729, A |
| 88 | 32 | 52.5 | 1125 | 4 | US-08-938-291A-5 | Sequence 5, Appl |
| 89 | 32 | 52.5 | 1244 | 3 | US-09-589-619-5 | Sequence 5, Appl |
| 90 | 32 | 52.5 | 1244 | 4 | US-09-252-991A-23150 | Sequence 23150, A |
| 91 | 32 | 52.5 | 1244 | 4 | US-08-093-453B-2 | Sequence 2, Appl |
| 92 | 32 | 52.5 | 2205 | 1 | US-09-252-991A-31366 | Sequence 31366, A |
| 93 | 31 | 51.6 | 376 | 4 | US-09-134-001C-4314 | Sequence 4314, Ap |
| 94 | 31 | 51.6 | 68 | 4 | US-09-252-991A-32788 | Sequence 32788, A |
| 95 | 31 | 50.8 | 806 | 4 | US-09-598-747-2 | Sequence 2, Appl |
| 96 | 31 | 50.8 | 119 | 4 | US-09-252-991A-22661 | Sequence 22661, A |
| 97 | 31 | 50.8 | 131 | 4 | US-09-252-991A-28746 | Sequence 28746, A |
| 98 | 31 | 50.8 | 187 | 4 | US-09-252-991A-26725 | Sequence 26725, A |
| 99 | 31 | 50.8 | 219 | 4 | US-09-252-991A-28381 | Sequence 28381, A |
| 100 | 31 | 50.8 | 228 | 4 | | |

ALIGNMENTS

RESULT 1
US-07-973-324A-4
Sequence 4, Application US/07973324A
Patent No. 5460952
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-4

Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDPRPYADG 10
|||||
DB 149 CRDD-PYGDG 157

RESULT 2
US-08-343-380-4
Sequence 4, Application US/08343380
Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,380
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-4

Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDPRPYADG 10
|||||
DB 149 CRDD-PYGDG 157

RESULT 3
US-09-072-435-4
Sequence 4, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match 68.0%; Score 41.5; DB 3; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRYADG 10
1111111111
DB 149 CRDD-PYGDG 157

RESULT 4
US-09-072-917A-4
Sequence 4, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 15
ADDRESS: Marshall, O'Toole, Garstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match 68.0%; Score 41.5; DB 3; Length 428;
Best Local Similarity 80.0%; Pred. No. 9.8;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDPRYADG 10
1111111111
DB 149 CRDD-PYGDG 157

RESULT 5
US-07-923-692C-6
Sequence 6, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 11
ADDRESS: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halliuh, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-6

Query Match 68.0%; Score 41.5; DB 1; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 CRDDPYADG 10
11111111
Db 155 CRDD-PYGDG 163

RESULT 6
US-08-184-237-6
Sequence 6, Application US/08184237
Patent No. 589367
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716

INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-6

Query Match 68.0%; Score 41.5; DB 1; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 CRDDPYADG 10
11111111
Db 155 CRDD-PYGDG 163

RESULT 7
US-08-482-920-6
Sequence 6, Application US/08482920
Patent No. 586785
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:

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? NAME: Halluin, Albert P.
? REGISTRATION NUMBER: 28,957
? REFERENCE/DOCKET NUMBER: 8129-112
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-854-3660
? TELEFAX: 415-854-3694
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 434 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-482-920-6

Query Match      68.0%; Score 41.5; DB 2; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches      8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1 CRDRPYADG 10
        1111 11 11
DB      155 CRDD-PYGDG 163

RESULT 8
US-08-484-341-6
? Sequence 6, Application US/08484341
? GENERAL INFORMATION:
? APPLICANT: Donson, Jon
? Dawson, William O.
? Grantham, George L.
? Turpen, Thomas H.
? Turpen, Ann Myers
? Garger, Stephen J.
? Grill, Laurence K.
? TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Limbach & Limbach
? STREET: 2001 Ferry Building
? CITY: San Francisco
? STATE: CAL
? ZIP: 94111
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,341
? FILING DATE: 07-Jun-1995
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/184,237
? FILING DATE: <Unknown>
? APPLICATION NUMBER: US 600,244
? FILING DATE: 22-OCT-1990
? APPLICATION NUMBER: US 641,617
? FILING DATE: 16-JAN-1991
? APPLICATION NUMBER: US 310,881
? FILING DATE: 17-FEB-1989
? APPLICATION NUMBER: US 160,766
? FILING DATE: 26-FEB-1988
? APPLICATION NUMBER: US 160,771
? FILING DATE: 26-FEB-1988
? APPLICATION NUMBER: US 347,637
? FILING DATE: 05-MAY-1989
? APPLICATION NUMBER: US 363,138
? FILING DATE: 08-JUN-1989
? APPLICATION NUMBER: US 219,279
? FILING DATE: 15-JUL-1988
? ATTORNEY/AGENT INFORMATION:
? NAME: Halluin, Albert P.
? REGISTRATION NUMBER: 28,957
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? REFERENCE/DOCKET NUMBER: BIOG-20121 USA
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-433-4150
? TELEFAX: 415-433-8716
? INFORMATION FOR SEQ ID NO: 6:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 434 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 6:
? US-08-484-341-6

Query Match      68.0%; Score 41.5; DB 3; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches      8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      1 CRDRPYADG 10
        1111 11 11
DB      155 CRDD-PYGDG 163

RESULT 9
US-08-483-502-6
? Sequence 6, Application US/08483502
? Patent No. 6284492
? GENERAL INFORMATION:
? APPLICANT: Donson, Jon
? Dawson, William O.
? Grantham, George L.
? Turpen, Thomas H.
? Turpen, Ann Myers
? Garger, Stephen J.
? Grill, Laurence K.
? TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Venable, Baetjer, Howard & Civiletti
? STREET: 1201 New York Avenue N.W., Suite 1000
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/483,502
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/739,143
? FILING DATE:
? APPLICATION NUMBER: US 600,244
? FILING DATE: 22-OCT-1990
? APPLICATION NUMBER: US 641,617
? FILING DATE: 16-JAN-1991
? APPLICATION NUMBER: US 310,881
? FILING DATE: 17-FEB-1989
? APPLICATION NUMBER: US 160,766
? FILING DATE: 26-FEB-1988
? APPLICATION NUMBER: US 160,771
? FILING DATE: 26-FEB-1988
? APPLICATION NUMBER: US 347,637
? FILING DATE: 05-MAY-1989
? PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 18604-090574
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-502-6

Query Match 68.0%; Score 41.5; DB 3; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
Db 155 CRDD-PYGDG 163

RESULT 10

US-09-726-651A-6
Sequence 6, Application US/09726651A

Patent No. 6448046

GENERAL INFORMATION:

APPLICANT: Dawson, Jon

APPLICANT: GRANTHAM, GEORGE L.

APPLICANT: TURPEN, Thomas H.

APPLICANT: TURPEN, Ann M.

APPLICANT: GARGER, Stephen J.

APPLICANT: GRILL, Laurence K.

TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS

FILE REFERENCE: 008010023CNS01

CURRENT APPLICATION NUMBER: US/09/726,651A

CURRENT FILING DATE: 2002-05-02

PRIOR APPLICATION NUMBER: 08/483,502

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/184,237

PRIOR FILING DATE: 1994-01-19

PRIOR APPLICATION NUMBER: 07/923,652

PRIOR FILING DATE: 1992-07-31

PRIOR APPLICATION NUMBER: 07/600,244

PRIOR FILING DATE: 1990-10-22

PRIOR APPLICATION NUMBER: 07/641,617

PRIOR FILING DATE: 1991-01-16

PRIOR APPLICATION NUMBER: 07/737,899

PRIOR FILING DATE: 1991-07-26

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 434

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: CLONE: alpha-amylase

OTHER INFORMATION: protein

US-09-726-651A-6

Query Match 68.0%; Score 41.5; DB 4; Length 434;
Best Local Similarity 80.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10

Db 155 CRDD-PYGDG 163

RESULT 11

US-09-252-991A-31890

Sequence 31890, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31890

LENGTH: 151

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-31890

Query Match 62.3%; Score 38; DB 4; Length 151;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10

Db 112 CRRSREPTDG 121

RESULT 12

US-09-252-991A-24086

Sequence 24086, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24086

LENGTH: 384

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24086

Query Match 62.3%; Score 38; DB 4; Length 384;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10

Db 37 CRADRPVAFG 46

RESULT 13

US-09-072-917A-9

Sequence 9, Application US/09072917A

Patent No. 6288302

GENERAL INFORMATION:

APPLICANT: Yu, Su-May

APPLICANT: Liu, Li-Fei

APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288102
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-9

Query Match 62.3%; Score 38; DB 3; Length 435;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
DB 148 CSDTOYSDG 157

RESULT 14
US-09-252-991A-19739
Sequence 19739, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19739
LENGTH: 500
TYPE: prt
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19739

Query Match 62.3%; Score 38; DB 4; Length 500;

Best Local Similarity 70.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDPRYADG 10
DB 340 CRDPRADG 349

RESULT 15
US-08-720-484A-5
Sequence 5, Application US/08720484A
Patent No. 5990281
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothed Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-720-484A-5

Query Match 62.3%; Score 38; DB 2; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPYADG 10
DB 68 RDKPWFDG 76

RESULT 16
US-08-953-823A-5
Sequence 5, Application US/08953823A
Patent No. 6136958
GENERAL INFORMATION:
APPLICANT: Desauvage, Frederic
APPLICANT: Rosenthal, Arnon
TITLE OF INVENTION: Vertebrate Smoothed Proteins
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION NUMBER: US/08/953,823A
; APPLICATION NUMBER: US/08/953,823A
; FILING DATE: 30-Sep-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027070
; FILING DATE: 30-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1050R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1036 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-953-823A-5

Query Match 62.3%; Score 38; DB 3; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPHYADG 10
Db 68 RDDKPWFDDG 76

RESULT 17
US-09-398-239-5
; Sequence 5, Application US/09398239
; Patent No. 6407216
; GENERAL INFORMATION:
; APPLICANT: Desauvage, Frederic
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Stone, Donna
; TITLE OF INVENTION: Vertebrate Smoothed Proteins
; FILE REFERENCE: P1050D1
; CURRENT APPLICATION NUMBER: US/09/398,239
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: US 08/720,484
; EARLIER FILING DATE: 1996-09-30
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-398-239-5

Query Match 62.3%; Score 38; DB 4; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPHYADG 10
Db 68 RDDKPWFDDG 76

RESULT 18
US-09-560-876A-5
; Sequence 5, Application US/09560876A
; Patent No. 6492139
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Rosenthal, Arnon

; APPLICANT: Stone, Donna
; TITLE OF INVENTION: Vertebrate Smoothed Proteins
; FILE REFERENCE: P1050R1D1
; CURRENT APPLICATION NUMBER: US/09/560,876A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/027,070
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: US 08/953,823
; PRIOR FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-560-876A-5

Query Match 62.3%; Score 38; DB 4; Length 1036;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPHYADG 10
Db 68 RDDKPWFDDG 76

RESULT 19
US-09-560-876A-6
; Sequence 6, Application US/09560876A
; Patent No. 6492139
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Stone, Donna
; TITLE OF INVENTION: Vertebrate Smoothed Proteins
; FILE REFERENCE: P1050R1D1
; CURRENT APPLICATION NUMBER: US/09/560,876A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/027,070
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: US 08/953,823
; PRIOR FILING DATE: 1997-09-30
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 6
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3
; OTHER INFORMATION: unknown amino acid
US-09-560-876A-6

Query Match 62.3%; Score 38; DB 4; Length 1065;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPHYADG 10
Db 97 RDDKPWFDDG 105

RESULT 20
US-09-328-352-7068
; Sequence 7068, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252

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; SEQ ID NO 7068
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7068

Query Match
Best Local Similarity 77.8%; Score 37; DB 4; Length 217;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
DB 185 RDDRPRYDYG 193

RESULT 21
US-08-991-862-17
; Sequence 17, Application US/08991862
; Patent No. 6309826
; GENERAL INFORMATION:
; APPLICANT: Seriero, Ginetle
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996.488/P001-A
; CURRENT FILING DATE: US/08/991.862
; EARLIER FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 CDNA
US-08-991-862-17

Query Match
Best Local Similarity 60.7%; Score 37; DB 4; Length 593;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDR-----PYADG 10
DB 534 CRDRNQCACCPYAG 549

RESULT 22
US-09-252-991A-22461
; Sequence 22461, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22461
; LENGTH: 588
; TYPE: PRT
; ORGANISM: pseudomonas aeruginosa
US-09-252-991A-22461

Query Match
Best Local Similarity 59.0%; Score 36; DB 4; Length 588;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDRPRYADG 10
DB 211 CRDRPRPRAAG 220

; SEQ ID NO 62
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-62

Query Match
Best Local Similarity 57.4%; Score 35; DB 4; Length 129;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDRPRYADG 10
DB 112 CRDRRLASG 121

RESULT 23
US-09-216-393B-62
; Sequence 62, Application US/09216393B
; Patent No. 6511694
; GENERAL INFORMATION:
; APPLICANT: Milhaussen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES T
; FILE REFERENCE: TX-1-C2
; CURRENT FILING DATE: US/09/216.393B
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393B-62

RESULT 24
US-08-965-689A-6
; Sequence 6, Application US/08965689A
; Patent No. 6015702
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,689A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 165 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 4257
US-08-965-689A-6

Query Match 57.4%; Score 35; DB 3; Length 165;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 DRPYADG 10
111111
Db 46 DTPYADG 52

RESULT 25

US-09-359-967-6
Sequence 6, Application US/09359967
Patent No. 6146624
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,689
FILING DATE:
APPLICATION NUMBER: 08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0356-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 4257
US-09-359-967-6

Query Match 57.4%; Score 35; DB 3; Length 165;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 DRPYADG 10
111111
Db 46 DTPYADG 52

RESULT 26
US-08-484-905-75
Sequence 75, Application US/08484905
Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-75

Query Match 57.4%; Score 35; DB 2; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 RDDRYADG 10
111111
Db 155 RDDRYADG 163

RESULT 27
US-08-481-985B-75
Sequence 75, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-75

Query Match 57.4%; Score 35; DB 3; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPPYADG 10
DB 155 RDDRAYLEG 163

RESULT 28
US-08-370-476-75
Sequence 75, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Koutilsky, Philippe
APPLICANT: Leme, Jo-Chun
APPLICANT: Ojcius, David
APPLICANT: Gastouge, Amanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-75

Query Match 57.4%; Score 35; DB 3; Length 306;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPPYADG 10
DB 155 RDDRAYLEG 163

RESULT 29
US-08-846-762-84
Sequence 84, Application US/08846762A
Patent No. 5994072
GENERAL INFORMATION:
APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: of O-antigen in Pseudomonas Aeruginosa
FILE REFERENCE: 6580-089
CURRENT APPLICATION NUMBER: US/08/846,762A
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
LENGTH: 362
TYPE: PRP
ORGANISM: Pseudomonas aeruginosa
US-08-846-762-84

Query Match 57.4%; Score 35; DB 2; Length 362;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPPYADG 10
DB 341 RDVOPYGDG 349

RESULT 30
US-09-252-991A-18424
Sequence 18424, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196, 136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ. ID NOS: 33142
; SEQ ID NO 18424
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18424

Query Match 57.4%; Score 35; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 3 DDRPYA 8
Db 198 DDRPYA 203

Search completed: August 29, 2003, 18:44:40
Job time : 11.5714 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:42:11 : Search time 15.7143 Seconds
(without alignments)
87.043 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDDRYADG 10

Scoring table:
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Gap 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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10: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US50_NEM_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US50_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-----------------------|-------------------|
| 1 | 41.5 | 68.0 | 740 | 12 US-10-280-679B-6 | Sequence 6, App1 |
| 2 | 38 | 62.3 | 740 | 15 US-10-156-761-6392 | Sequence 8392, Ap |
| 3 | 37 | 60.7 | 118 | 15 US-10-155-886-40 | Sequence 40, App1 |
| 4 | 37 | 60.7 | 293 | 15 US-10-155-886-11 | Sequence 11, App1 |
| 5 | 37 | 60.7 | 413 | 15 US-10-097-340-141 | Sequence 141, App |
| 6 | 37 | 60.7 | 593 | 9 US-09-813-156-17 | Sequence 17, App1 |
| 7 | 37 | 60.7 | 593 | 9 US-09-824-807-17 | Sequence 17, App1 |
| 8 | 37 | 60.7 | 593 | 10 US-09-824-647-17 | Sequence 17, App1 |
| 9 | 37 | 60.7 | 593 | 15 US-10-218-509-17 | Sequence 17, App1 |
| 10 | 37 | 60.7 | 593 | 15 US-10-281-160-17 | Sequence 17, App1 |
| 11 | 37 | 60.7 | 771 | 9 US-09-784-358-14 | Sequence 14, App1 |
| 12 | 37 | 60.7 | 845 | 9 US-09-784-358-12 | Sequence 12, App1 |
| 13 | 37 | 60.7 | 1023 | 11 US-09-789-390-25 | Sequence 25, App1 |
| 14 | 37 | 60.7 | 1023 | 11 US-09-789-390-27 | Sequence 27, App1 |
| 15 | 37 | 60.7 | 1023 | 11 US-09-789-390-28 | Sequence 28, App1 |

| | | | | | |
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| 16 | 37 | 60.7 | 1023 | 11 US-09-789-390-59 | Sequence 59, App1 |
| 17 | 37 | 60.7 | 1023 | 11 US-09-789-390-61 | Sequence 61, App1 |
| 18 | 37 | 60.7 | 1281 | 11 US-09-789-390-2 | Sequence 2, App1 |
| 19 | 37 | 60.7 | 1281 | 11 US-09-789-390-5 | Sequence 5, App1 |
| 20 | 37 | 60.7 | 1617 | 9 US-09-784-358-16 | Sequence 16, App1 |
| 21 | 37 | 60.7 | 1691 | 9 US-09-784-358-2 | Sequence 2, App1 |
| 22 | 37 | 60.7 | 1691 | 11 US-09-789-390-4 | Sequence 4, App1 |
| 23 | 36 | 59.0 | 246 | 9 US-09-815-242-10983 | Sequence 10983, A |
| 24 | 36 | 59.0 | 255 | 9 US-09-815-242-10261 | Sequence 10261, A |
| 25 | 36 | 59.0 | 255 | 9 US-09-815-242-14085 | Sequence 14085, A |
| 26 | 36 | 59.0 | 4834 | 15 US-10-156-761-7849 | Sequence 7849, Ap |
| 27 | 36 | 59.0 | 4834 | 15 US-10-156-761-7849 | Sequence 7849, Ap |
| 28 | 36 | 59.0 | 4834 | 15 US-10-156-761-7849 | Sequence 7849, Ap |
| 29 | 35.5 | 58.2 | 129 | 9 US-09-934-455-200 | Sequence 200, App |
| 30 | 35.5 | 58.2 | 129 | 9 US-09-934-455-200 | Sequence 14, App1 |
| 31 | 35 | 57.4 | 165 | 15 US-10-157-669-33 | Sequence 33, App1 |
| 32 | 35 | 57.4 | 165 | 15 US-10-157-669-33 | Sequence 33, App1 |
| 33 | 35 | 57.4 | 554 | 10 US-09-738-626-6289 | Sequence 6289, Ap |
| 34 | 35 | 57.4 | 775 | 15 US-10-156-761-12824 | Sequence 12824, A |
| 35 | 34 | 55.7 | 117 | 15 US-10-155-886-42 | Sequence 42, App1 |
| 36 | 34 | 55.7 | 235 | 15 US-10-155-886-12 | Sequence 12, App1 |
| 37 | 34 | 55.7 | 922 | 15 US-10-156-761-14719 | Sequence 14719, A |
| 38 | 34 | 55.7 | 922 | 15 US-10-128-714-3524 | Sequence 3524, Ap |
| 39 | 34 | 55.7 | 949 | 15 US-10-128-714-8524 | Sequence 8524, Ap |
| 40 | 33 | 54.1 | 30 | 9 US-09-864-761-33683 | Sequence 33683, A |
| 41 | 33 | 54.1 | 177 | 15 US-10-156-761-12737 | Sequence 12737, A |
| 42 | 33 | 54.1 | 259 | 15 US-10-304-928-18 | Sequence 18, App1 |
| 43 | 33 | 54.1 | 361 | 15 US-10-156-761-9961 | Sequence 9961, Ap |
| 44 | 33 | 54.1 | 439 | 12 US-10-228-063-51 | Sequence 51, App1 |
| 45 | 33 | 54.1 | 439 | 15 US-10-156-761-8346 | Sequence 8346, Ap |
| 46 | 33 | 54.1 | 496 | 10 US-09-312-762A-15 | Sequence 15, App1 |
| 47 | 33 | 54.1 | 532 | 15 US-10-156-761-10868 | Sequence 10868, A |
| 48 | 33 | 54.1 | 733 | 15 US-10-138-927-77 | Sequence 77, App1 |
| 49 | 32.5 | 53.3 | 203 | 15 US-10-156-761-11347 | Sequence 11347, A |
| 50 | 32.5 | 52.5 | 66 | 15 US-10-000-256A-201 | Sequence 201, App |
| 51 | 32 | 52.5 | 71 | 15 US-10-156-761-10479 | Sequence 10479, A |
| 52 | 32 | 52.5 | 105 | 9 US-09-764-877-1863 | Sequence 1863, Ap |
| 53 | 32 | 52.5 | 139 | 9 US-09-658-20 | Sequence 20, App1 |
| 54 | 32 | 52.5 | 139 | 9 US-09-844-353A-20 | Sequence 20, App1 |
| 55 | 32 | 52.5 | 147 | 9 US-09-925-302-451 | Sequence 451, App |
| 56 | 32 | 52.5 | 148 | 15 US-10-156-761-14866 | Sequence 14866, A |
| 57 | 32 | 52.5 | 153 | 15 US-10-156-761-7581 | Sequence 7581, Ap |
| 58 | 32 | 52.5 | 153 | 15 US-10-156-761-7581 | Sequence 7581, Ap |
| 59 | 32 | 52.5 | 202 | 11 US-09-924-600A-62 | Sequence 62, App1 |
| 60 | 32 | 52.5 | 202 | 11 US-09-924-600A-62 | Sequence 62, App1 |
| 61 | 32 | 52.5 | 202 | 11 US-09-924-600A-62 | Sequence 62, App1 |
| 62 | 32 | 52.5 | 202 | 11 US-09-924-600A-62 | Sequence 62, App1 |
| 63 | 32 | 52.5 | 202 | 15 US-10-000-489-62 | Sequence 62, App1 |
| 64 | 32 | 52.5 | 202 | 15 US-10-000-489-62 | Sequence 62, App1 |
| 65 | 32 | 52.5 | 236 | 9 US-09-815-242-11820 | Sequence 11820, A |
| 66 | 32 | 52.5 | 252 | 9 US-09-815-242-11946 | Sequence 11946, A |
| 67 | 32 | 52.5 | 324 | 10 US-09-816-095-4 | Sequence 4, App1 |
| 68 | 32 | 52.5 | 328 | 15 US-10-156-761-12842 | Sequence 12842, A |
| 69 | 32 | 52.5 | 416 | 15 US-10-128-714-3579 | Sequence 3579, Ap |
| 70 | 32 | 52.5 | 423 | 14 US-10-062-254-358 | Sequence 358, App |
| 71 | 32 | 52.5 | 423 | 15 US-10-128-714-8223 | Sequence 8223, Ap |
| 72 | 32 | 52.5 | 428 | 15 US-10-128-714-8579 | Sequence 8579, Ap |
| 73 | 32 | 52.5 | 510 | 10 US-09-369-735B-7 | Sequence 7, App1 |
| 74 | 32 | 52.5 | 510 | 14 US-10-121-032-22 | Sequence 22, App1 |
| 75 | 32 | 52.5 | 510 | 15 US-10-093-037-22 | Sequence 22, App1 |
| 76 | 32 | 52.5 | 516 | 10 US-09-738-626-6665 | Sequence 6665, Ap |
| 77 | 32 | 52.5 | 542 | 11 US-10-156-761-14592 | Sequence 14592, A |
| 78 | 32 | 52.5 | 617 | 11 US-09-866-050A-303 | Sequence 303, App |
| 79 | 32 | 52.5 | 621 | 9 US-09-925-301-1416 | Sequence 1416, App |
| 80 | 32 | 52.5 | 751 | 10 US-09-738-626-6525 | Sequence 6525, Ap |
| 81 | 31 | 50.8 | 50 | 9 US-09-864-761-44719 | Sequence 44719, A |
| 82 | 31 | 50.8 | 90 | 9 US-09-925-297-676 | Sequence 676, App |
| 83 | 31 | 50.8 | 105 | 11 US-09-764-891-3191 | Sequence 3191, App |
| 84 | 31 | 50.8 | 110 | 12 US-10-306-292-2 | Sequence 2, App1 |
| 85 | 31 | 50.8 | 119 | 10 US-09-893-737-144 | Sequence 144, App |
| 86 | 31 | 50.8 | 158 | 10 US-09-764-868-948 | Sequence 948, App |
| 87 | 31 | 50.8 | 179 | 15 US-10-156-761-11443 | Sequence 11443, A |
| 88 | 31 | 50.8 | 182 | 12 US-10-181-590-7 | Sequence 7, App1 |

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89      31      50.8      200      9      US-09-734-569-138      Sequence 138, App
90      31      50.8      222      9      US-09-815-242-13842      Sequence 13842, A
91      31      50.8      238      15      US-10-153-668-264      Sequence 264, App
92      31      50.8      239      9      US-09-815-242-13417      Sequence 13417, A
93      31      50.8      239      9      US-09-815-242-13569      Sequence 13569, A
94      31      50.8      239      11      US-09-929-769-6      Sequence 6, Appl
95      31      50.8      239      11      US-09-946-374-324      Sequence 324, App
96      31      50.8      239      12      US-10-015-387A-324      Sequence 324, App
97      31      50.8      239      12      US-10-006-130A-324      Sequence 324, App
98      31      50.8      239      12      US-10-199-672-354      Sequence 354, App
99      31      50.8      239      12      US-10-006-172A-324      Sequence 324, App
100     31      50.8      239      12      US-10-187-749-354      Sequence 354, App
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ALIGNMENTS

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RESULT 1
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; Sequence 6, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
; FILE REFERENCE: LSRC-0109-US03
; CURRENT APPLICATION NUMBER: US/10/280,679B
; CURRENT FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Rice alpha-amylase
US-10-280-679B-6

Query Match      68.0%; Score 41.5; DB 12; Length 434;
Best Local Similarity 80.0%; Pred. No. 16;
Matches      8; Conservative      0; Mismatches      1; Indels      1; Gaps      1;
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Oy      1      CRDPRYADG 10
Db      155      CRDP-PTGDDG 163
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RESULT 2
US-10-156-761-8392
; Sequence 8392, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
```

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; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKABI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8392
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8392
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Best Local Similarity 66.7%; Pred. No. 1,2e+02;
Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
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Oy      2      RDPRPYADG 10
Db      717      REDTPYGDG 725
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RESULT 3
US-10-155-886-40
; Sequence 40, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kernani, Pouneth
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-155-886-40

Query Match      60.7%; Score 37; DB 15; Length 118;
Best Local Similarity 60.0%; Pred. No. 26;
Matches      6; Conservative      1; Mismatches      3; Indels      0; Gaps      0;
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Oy      1      CRDPRYADG 10
Db      57      CRDPRVSSG 66
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RESULT 4
US-10-155-886-11
; Sequence 11, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kernani, Pouneth
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-09-824-647-17

Query Match 60.7%; Score 37; DB 10; Length 593;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDDR-----PYADG 10
Db 534 CRDNRQGWACCPYAOG 549

RESULT 9
; Sequence 17, Application US/10218509
; Publication No. US20030092661A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996,488/P001-A
; CURRENT APPLICATION NUMBER: US/10/218,509
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-10-218-509-17

Query Match 60.7%; Score 37; DB 15; Length 593;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDDR-----PYADG 10
Db 534 CRDNRQGWACCPYAOG 549

RESULT 10
US-10-281-160-17
; Sequence 17, Application US/10281160
; Publication No. US20030108950A1
; GENERAL INFORMATION:
; APPLICANT: Serrero, GINETTE
; TITLE OF INVENTION: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS
; FILE REFERENCE: 29996,488/P001-A
; CURRENT APPLICATION NUMBER: US/10/281,160
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/08/991,862
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/863,862
; PRIOR FILING DATE: 1997-05-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 17
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human GP88 cDNA
US-10-281-160-17

Query Match 60.7%; Score 37; DB 15; Length 593;

Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

QY 1 CRDDR-----PYADG 10
Db 534 CRDNRQGWACCPYAOG 549

RESULT 11
US-09-784-358-14
; Sequence 14, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; FILE REFERENCE: LEX-0134-USA
; CURRENT APPLICATION NUMBER: US/09/784,358
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,282
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 771
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-14

Query Match 60.7%; Score 37; DB 9; Length 771;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRXYA 8
Db 669 CRDEKPHA 676

RESULT 12
US-09-784-358-12
; Sequence 12, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; FILE REFERENCE: LEX-0134-USA
; CURRENT APPLICATION NUMBER: US/09/784,358
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/183,282
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 845
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-12

Query Match 60.7%; Score 37; DB 9; Length 845;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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      11111111
DB      743 CRDEKPHA 750

RESULT 13
US-09-789-390-25
; Sequence 25, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-25

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
DB      75 CRDEKPHA 82

RESULT 14
US-09-789-390-27
; Sequence 27, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
DB      75 CRDEKPHA 82

RESULT 15
US-09-789-390-28
; Sequence 28, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-28

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY      1 CRDDRPA 8
      11111111
DB      75 CRDEKPHA 82

RESULT 16
US-09-789-390-59
; Sequence 59, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-59

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRDDRPYA 8
        |||::|:|
Db      75 CRDEKPHA 82

RESULT 17
US-09-789-390-61
; Sequence 61, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-61

Query Match      60.7%; Score 37; DB 11; Length 1023;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRDDRPYA 8
        |||::|:|
Db      75 CRDEKPHA 82

RESULT 18
US-09-789-390-2
; Sequence 2, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
US-09-789-390-2
```

```

; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-2

Query Match      60.7%; Score 37; DB 11; Length 1281;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRDDRPYA 8
        |||::|:|
Db      333 CRDEKPHA 340

RESULT 19
US-09-789-390-5
; Sequence 5, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT APPLICATION NUMBER: US/09/789,390
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185,548
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/199,957
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/184,951
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 60/185,967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/197,723
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-5

Query Match      60.7%; Score 37; DB 11; Length 1281;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CRDDRPYA 8
        |||::|:|
Db      333 CRDEKPHA 340
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```
RESULT 20
US-09-784-358-16
; Sequence 16, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; FILE REFERENCE: LEX-0134-USA
; CURRENT FILING DATE: 2001-02-15
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1617
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-16

Query Match      60.7%; Score 37; DB 9; Length 1617;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CRDRPYA 8
Db      669 CRDEKPA 676

RESULT 21
US-09-784-358-2
; Sequence 2, Application US/09784358
; Patent No. US20020099027A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NOVEL HUMAN THROMBOSPONDIN REPEAT PROTEINS AND
; FILE REFERENCE: LEX-0134-USA
; CURRENT FILING DATE: 2001-02-15
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1691
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-784-358-2

Query Match      60.7%; Score 37; DB 9; Length 1691;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CRDRPYA 8
Db      743 CRDEKPA 750

RESULT 22
US-09-789-390-4
; Sequence 4, Application US/09789390
; Publication No. US20030059768A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: MacDougall, John
; APPLICANT: Shinkels, Richard A
; APPLICANT: Spaderna, Steven K
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-692
; CURRENT FILING DATE: 2001-02-23
; PRIOR FILING DATE: 2000-02-28
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-02-25
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-03-01
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-390-4

Query Match      60.7%; Score 37; DB 11; Length 1691;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      1 CRDRPYA 8
Db      743 CRDEKPA 750

RESULT 23
US-09-813-242-10983
; Sequence 10983, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10983
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LENGTH: 246
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-815-242-10983

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 246;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 24
US-09-815-242-10261
Sequence 10261, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10261
LENGTH: 255
TYPE: PRT
ORGANISM: Escherichia coli

US-09-815-242-10261

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 25
US-09-815-242-14085

Sequence 14085, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14085
LENGTH: 255
TYPE: PRT
ORGANISM: Salmonella typhi

US-09-815-242-14085

Query Match
Best Local Similarity 59.0%; Score 36; DB 9; Length 255;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
|||||
Db 50 DDRPYGGG 57

RESULT 26
US-10-156-761-7849

Sequence 7849, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7849
LENGTH: 353
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-7849

Query Match
Best Local Similarity 59.0%; Score 36; DB 15; Length 353;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RDDRPY 7
|||||
Db 264 RDDRPY 269

```
RESULT 27
US-10-097-534-27
; Sequence 27, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 4834
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-534-27

Query Match      59.0%; Score 36; DB 15; Length 4834;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CRDPRYADG 10
      ||| |:::|
DB      349 CRDAPHSEG 358

RESULT 28
US-09-934-455-200
; Sequence 200, Application US/09934455
; Publication No. US20030121070A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Kedzie, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Plineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-200
```

```
Query Match      58.2%; Score 35.5; DB 11; Length 280;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1 CRDP-PPYADG 10
      ||| |:::|
DB      194 CNDDETPYVDG 204

RESULT 29
US-10-233-926-14
; Sequence 14, Application US/10233926
; Publication No. US2003013182A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Falco, S. Carl
; TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLYLTRANSFERASE
; FILE REFERENCE: BB1419 US NA
; CURRENT APPLICATION NUMBER: US/10/233,926
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US/09/735,846
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Zea mays
US-10-233-926-14

Query Match      58.2%; Score 35.5; DB 16; Length 328;
Best Local Similarity 72.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY      3 DDRP--YADG 10
      ||| |:::|
DB      72 DDRPVRVYADG 82

RESULT 30
US-09-216-393-62
; Sequence 62, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOMOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/994,825
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393-62

Query Match      57.4%; Score 35; DB 9; Length 129;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRDPRYADG 10
      ||| |:::|
DB      112 CRDERELASG 121

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Job time : 17.7143 secs
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 10.2857 Seconds
(without alignments)
93.497 Million cell updates/sec

Title: US-09-830-876-2

Perfect score: 61

Sequence: 1 CRDDPRYADG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 56 | 91 | 8 | 429 1 | JR0406 |
| 3 | 44 | 72 | 1 | 431 2 | S10514 |
| 4 | 44 | 72 | 1 | 437 2 | S07040 |
| 5 | 44 | 72 | 1 | 438 1 | ALBH |
| 6 | 41.5 | 68 | 0 | 428 2 | S10013 |
| 7 | 41.5 | 68 | 0 | 424 2 | S12775 |
| 8 | 41 | 67 | 2 | 121 2 | S04123 |
| 9 | 41 | 67 | 2 | 151 2 | B93345 |
| 10 | 41 | 67 | 2 | 278 2 | T03440 |
| 11 | 41 | 67 | 2 | 423 2 | T09942 |
| 12 | 41 | 67 | 2 | 1469 2 | T24216 |
| 13 | 40 | 65 | 6 | 248 2 | AE0281 |
| 14 | 40 | 65 | 6 | 443 2 | J01527 |
| 15 | 40 | 65 | 6 | 445 2 | S19990 |
| 16 | 39 | 63 | 9 | 144 2 | H70971 |
| 17 | 39 | 63 | 9 | 370 2 | AB7358 |
| 18 | 38 | 62 | 3 | 153 2 | J01648 |
| 19 | 38 | 62 | 3 | 373 2 | T43962 |
| 20 | 38 | 62 | 3 | 386 2 | T44151 |
| 21 | 38 | 62 | 3 | 386 2 | T44151 |
| 22 | 38 | 62 | 3 | 386 2 | T44151 |
| 23 | 38 | 62 | 3 | 386 2 | T44151 |
| 24 | 38 | 62 | 3 | 386 2 | T44151 |
| 25 | 37 | 60 | 7 | 243 2 | A26311 |
| 26 | 37 | 60 | 7 | 253 1 | C47031 |
| 27 | 37 | 60 | 7 | 325 2 | T11610 |
| 28 | 37 | 60 | 7 | 463 2 | T29442 |
| 29 | 37 | 60 | 7 | 521 2 | F87317 |
| 30 | 37 | 60 | 7 | 546 1 | S71008 |

| | | | | | | |
|-----|------|------|------|---|--------|----------------------|
| 30 | 36 | 59.0 | 237 | 2 | C84976 | tRNA (guanine-N1-) |
| 31 | 36 | 59.0 | 246 | 2 | C64054 | tRNA (guanine-N1-) |
| 32 | 36 | 59.0 | 246 | 2 | A10399 | tRNA (guanine-N1-) |
| 33 | 36 | 59.0 | 255 | 1 | XYECG1 | tRNA (guanine-N1-) |
| 34 | 36 | 59.0 | 255 | 2 | S37175 | tRNA (guanine-N1-) |
| 35 | 36 | 59.0 | 255 | 2 | B85907 | tRNA (guanine-N1-) |
| 36 | 36 | 59.0 | 255 | 2 | F91062 | tRNA (guanine-N1-) |
| 37 | 36 | 59.0 | 255 | 2 | AF0833 | tRNA (guanine-N1-) |
| 38 | 36 | 59.0 | 282 | 2 | T35294 | probable endo alpn |
| 39 | 36 | 59.0 | 423 | 2 | T15350 | hypothetical prote |
| 40 | 36 | 59.0 | 440 | 2 | S14958 | alpha-amylase (EC |
| 41 | 36 | 59.0 | 516 | 2 | H87233 | probable secreted |
| 42 | 36 | 59.0 | 1123 | 2 | T19713 | hypothetical prote |
| 43 | 35.5 | 58.2 | 206 | 2 | T51656 | probable transcrip |
| 44 | 35.5 | 58.2 | 280 | 2 | T49501 | alpha-xylosidase - |
| 45 | 35.5 | 58.2 | 764 | 2 | A72394 | hypothetical prote |
| 46 | 35 | 57.4 | 85 | 2 | F69933 | hypothetical prote |
| 47 | 35 | 57.4 | 153 | 2 | T31701 | ubiquitin-conjugat |
| 48 | 35 | 57.4 | 165 | 2 | S28951 | neutrontal growth-re |
| 49 | 35 | 57.4 | 196 | 2 | B84638 | neutromodulin - mou |
| 50 | 35 | 57.4 | 226 | 2 | A26964 | limb protein - Str |
| 51 | 35 | 57.4 | 227 | 2 | A29800 | hypothetical prote |
| 52 | 35 | 57.4 | 227 | 2 | S44973 | hypothetical prote |
| 53 | 35 | 57.4 | 362 | 2 | S70675 | probable alkaline |
| 54 | 35 | 57.4 | 443 | 2 | T08905 | hypothetical prote |
| 55 | 35 | 57.4 | 469 | 2 | T36441 | hypothetical prote |
| 56 | 35 | 57.4 | 553 | 2 | T36441 | hypothetical prote |
| 57 | 35 | 57.4 | 579 | 2 | A84227 | hypothetical prote |
| 58 | 35 | 57.4 | 659 | 2 | S36551 | hypothetical prote |
| 59 | 35 | 56.6 | 191 | 2 | F72731 | hypothetical prote |
| 60 | 34 | 55.7 | 164 | 2 | T35949 | hypothetical prote |
| 61 | 34 | 55.7 | 172 | 2 | T34464 | hypothetical prote |
| 62 | 34 | 55.7 | 235 | 2 | S14481 | hypothetical prote |
| 63 | 34 | 55.7 | 260 | 2 | B82362 | hypothetical prote |
| 64 | 34 | 55.7 | 309 | 2 | AF0746 | hypothetical prote |
| 65 | 34 | 55.7 | 315 | 2 | T44480 | conserved hypotet |
| 66 | 34 | 55.7 | 332 | 2 | T51269 | hypothetical prote |
| 67 | 34 | 55.7 | 356 | 2 | T30361 | occlusion-derived |
| 68 | 34 | 55.7 | 393 | 2 | S54541 | BDI protein - yea |
| 69 | 34 | 55.7 | 435 | 2 | AD3255 | alpha-amylase (EC |
| 70 | 34 | 55.7 | 494 | 2 | AD3255 | l-sorbose dehydrog |
| 71 | 34 | 55.7 | 513 | 2 | T30733 | A-type inclusion b |
| 72 | 34 | 55.7 | 545 | 2 | AH2430 | Crp synthetase [im |
| 73 | 34 | 55.7 | 548 | 2 | C84352 | lysyl-tRNA synthet |
| 74 | 34 | 55.7 | 661 | 2 | F90360 | hypothetical prote |
| 75 | 34 | 55.7 | 704 | 2 | T31327 | tRNA protein hemol |
| 76 | 34 | 55.7 | 759 | 2 | S5136 | glycogen(starch) s |
| 77 | 34 | 55.7 | 759 | 2 | F70539 | probable 5-methyl |
| 78 | 34 | 55.7 | 760 | 2 | C87029 | hypothetical prote |
| 79 | 34 | 55.7 | 1007 | 2 | H72734 | hypothetical prote |
| 80 | 34 | 55.7 | 1166 | 2 | F96598 | hypothetical prote |
| 81 | 33.5 | 54.9 | 175 | 2 | T35455 | hypothetical prote |
| 82 | 33 | 54.1 | 109 | 2 | C84357 | hypothetical prote |
| 83 | 33 | 54.1 | 123 | 2 | S30532 | Ig heavy chain V r |
| 84 | 33 | 54.1 | 198 | 2 | H81254 | probable permease |
| 85 | 33 | 54.1 | 224 | 2 | E72704 | hypothetical prote |
| 86 | 33 | 54.1 | 224 | 2 | A95394 | hypothetical prote |
| 87 | 33 | 54.1 | 228 | 2 | S38382 | SEB4B protein - hu |
| 88 | 33 | 54.1 | 229 | 2 | S38383 | SEB4B protein - hu |
| 89 | 33 | 54.1 | 237 | 2 | S38384 | SEB4B protein - mou |
| 90 | 33 | 54.1 | 244 | 2 | T15647 | hypothetical prote |
| 91 | 33 | 54.1 | 247 | 2 | C82307 | tRNA (guanine-N1-) |
| 92 | 33 | 54.1 | 247 | 2 | T17677 | hypothetical prote |
| 93 | 33 | 54.1 | 247 | 2 | T33034 | hypothetical prote |
| 94 | 33 | 54.1 | 248 | 2 | H86153 | probable chitinase |
| 95 | 33 | 54.1 | 272 | 2 | T86153 | uncharacterized pr |
| 96 | 33 | 54.1 | 283 | 2 | G96979 | uroporphyrin-III C |
| 97 | 33 | 54.1 | 306 | 2 | JC4347 | chemotaxis protein |
| 98 | 33 | 54.1 | 308 | 1 | G90953 | chemotaxis protein |
| 99 | 33 | 54.1 | 308 | 1 | G90953 | chemotaxis protein |
| 100 | 33 | 54.1 | 308 | 2 | C85802 | hypothetical prote |

ALIGNMENTS

RESULT 1

ALBHB

alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2

C:Species: Hordeum vulgare (barley)

C>Date: 30-Jun-1987 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999

C:Accession: A31960; A00847; J0405; A26267; A24457; A30759

R:Khurshed, B.; Rogers, J.C.

J: Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA levels

A:Reference number: A92700; MUID:8906691; PMID:3264283

A:Accession: A31960

A:Molecule type: DNA

A:Residues: 1-427 <KHU>

A:Cross-references: GB:J04262

A:Experimental source: cv. Himalaya; gene Amy6-4

R:Rogers, J.C.

J: Biol. Chem. 260, 3731-3738, 1985

A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone cell

A:Reference number: A00847; MUID:85131184; PMID:3871776

A:Accession: A00847

A:Molecule type: mRNA

A:Residues: 1-133,'D',135-194,'HRL',198-424,'Q',426-427 <ROG>

A:Experimental source: seed

R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan

Plant Mol. Biol. 12, 119-121, 1989

A:Title: Nucleotide and predicted amino acid sequences of two different genes for high- α -D-glucanase

A:Reference number: J0405

A:Accession: J0405

A:Molecule type: DNA

A:Residues: 1-133,'D',135-424,'Q',426-427 <RAH>

A:Cross-references: EMBL:X15226; NID:918894; PDB:CAA33299.1; PID:g295804

A:Experimental source: gene Amy152

R:Chandler, P.M.; Zwart, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Ingalls, A.S.

Plant Mol. Biol. 3, 407-418, 1984

A:Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels

A:Reference number: A26267

A:Accession: A26267

A:Molecule type: mRNA

A:Residues: 1-133,'V',135-184,'A',186-366,'GA' <CHN>

A:Experimental source: cv. Himalaya

A>Note: the authors translated the codon GTC for residue 134 as Gly

R:Svensson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.

Carlsberg Res. Commun. 50, 15-22, 1985

A:Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.

A:Reference number: A24457

A:Accession: A24457

A:Molecule type: protein

A:Residues: 25-59,'X',61-67,'HX',70-85,'X',87-92,'E',94,146-165,228-251,297-303,'X',305-

C:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated and

ed by the embryo during germination.

C:Genetics:

A:Gene: Amy2-2

A:Map position: 6

A:Introns: 29/3; 344/3

A>Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-amylase

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosidase;

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-427/Product: alpha-amylase #status experimental <MAT>

F:170-316/Domain: alpha-amylase core homology <AMY>

F:25/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carb

F:203,228,313/Active site: Asp, Glu, Asp #status predicted

QY 1 CRDDPRYADG 10
Db 148 CRDDPRYADG 157

RESULT 2

alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley

N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C:Species: Hordeum vulgare (barley)

C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999

C:Accession: J0406; B30759; S06275; B31960; B21826

R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan

Plant Mol. Biol. 12, 119-121, 1989

A:Title: Nucleotide and predicted amino acid sequences of two different genes for high- α -D-glucanase

A:Reference number: J0405

A:Accession: J0406

A:Molecule type: DNA

A:Residues: 1-429 <RAH>

A:Cross-references: EMBL:X15227; NID:918899; PDB:CAA33299.1; PID:g295805

A:Experimental source: gene Amy56 for alpha-amylase

A:Genetics: A56

R:Rogers, J.C.

submitted to GenBank, September 1988

A:Reference number: A94535

A:Accession: B30759

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-39

A:Cross-references: GB:J04262; NID:9166984; PDB:AAA98615.1; PID:g166985

A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B

A:Genetics: A46

R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.

Plant Mol. Biol. 9, 3-17, 1987

A:Title: Structure and organization of two divergent alpha-amylase genes from barley.

A:Reference number: S06275

A:Accession: S06275

A:Molecule type: DNA

A:Residues: 1-11,'L',14-32,'S',34-57,'T',59-79,'Y',81-139,'R',141-160,'PA',163-164,'

A:Cross-references: EMBL:M17125; NID:9166978; PDB:AAA32926.1; PID:g166979

A:Experimental source: cv. Sundance gene for alpha-amylase 1 precursor (clone p141.11

A:Genetics: A41

A>Note: the authors translated the codon TCG for residue 33 as Trp

R:Khurshed, B.; Rogers, J.C.

J: Biol. Chem. 263, 18953-18960, 1988

A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA lev

A:Reference number: A92700; MUID:8906691; PMID:3264283

A:Accession: B31960

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-51 <KHU>

A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor

R:Huang, J.K.; Sweigle, M.; Dandekar, A.M.; Muthukrishnan, S.

J. Mol. Appl. Genet. 2, 579-588, 1984

A:Reference number: A92837; MUID:85159405; PMID:6335720

A:Accession: B21826

A:Molecule type: mRNA

A:Residues: 379-389,'T',391-392,'D',394-429 <HUA>

A:Cross-references: GB:K02636; NID:9166992; PDB:AAA29932.1; PID:g166993

A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)

C:Genetics: <A56>

A:Gene: Amy56

A:Introns: 29/3; 346/3

C:Genetics: <A46>

A:Gene: Amy46

C:Genetics: <A41>

A:Gene: Amy1

A:Map position: 6

A:Introns: 29/3; 346/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

Query Match 100.0%; Score 61; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: aleurone cell; germination; glycosidase; hydrolase; polysaccharide degradat
 F:172-318/Domain: alpha-amylase core homology <AMY>
 F:205,230,315/Active site: Asp, Glu, Asp #status predicted

Query Match 91.8%; Score 56; DB 1; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.0096;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 148 CRDDRPYDGS 157

RESULT 3

alpha-amylase (EC 3.2.1.1) precursor - black gram
 S10514
 C:Species: Vigna mungo (black gram)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10514; S61336; S40201; S61334
 R:Yamauchi, D.; Minamikawa, T.
 Nucleic Acids Res. 18, 4250, 1990
 A:Title: Nucleotide sequence of cDNA for alpha-amylase from cotyledons of germinating Vi
 A:Reference number: S10514; MUID:90332425; PMID:2377468
 A:Accession: S10514
 A:Molecule type: mRNA
 A:Residues: 1-421 <YAM>
 A:Cross-references: EMBL:X53049; NID:g22059; PIDN:CAA37217.1; PID:g22060
 A:Accession: S61336
 A:Molecule type: protein
 A:Residues: 24-31 <YAM>
 R:Ratensch, H.; Yamauchi, D.; Wada, S.; Minamikawa, T.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Nucleotide sequence of the alpha-amylase gene from Vigna mungo.
 A:Reference number: S40201
 A:Accession: S40201
 A:Molecule type: DNA
 A:Residues: 1-421 <TAM>
 A:Cross-references: EMBL:X73301; NID:g437944; PIDN:CAA51734.1; PID:g437945
 C:Genetic references: EMBL:X73301; NID:g437944; PIDN:CAA51734.1; PID:g437945
 A:Introns: 28/3; 72/1; 340/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-421/Product: alpha-amylase #status predicted <AMT>
 F:168-312/Domain: alpha-amylase core homology <AMY>
 F:201,226,309/Active site: Asp, Glu, Asp #status predicted

Query Match 72.1%; Score 44; DB 2; Length 421;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 146 CRDDRPYDGS 155

RESULT 4

alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley
 S07040
 C:Species: Hordeum vulgare (barley)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 22-Jun-1999
 C:Accession: S07040
 R:Knorr, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
 Plant Mol Biol. 9, 3-17, 1987
 A:Title: Structure and organization of two divergent alpha-amylase genes from barley.
 A:Reference number: S06275
 A:Accession: S07040
 A:Molecule type: DNA
 A:Residues: 1-437 <KNO>

A:Cross-references: EMBL:M17127; NID:g166982; PIDN:AAA32928.1; PID:g166983
 C:Genetics:
 A:Gene: amy2
 A:Map position: 1
 A:Introns: 29/3; 74/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMY>
 F:203,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 72.1%; Score 44; DB 2; Length 437;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 148 CRDDRPYDGS 157

RESULT 5

alpha-amylase (EC 3.2.1.1) precursor - barley
 ALBH
 C:Species: Hordeum vulgare (barley)
 C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999
 C:Accession: A00846; S65602
 R:Rogers, J.C.; Milliman, C.
 J. Biol. Chem. 258, 8169-8174, 1983
 A:Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
 A:Reference number: A00846; MUID:83238423; PMID:6150808
 A:Accession: A00846
 A:Molecule type: mRNA
 A:Residues: 1-438 <ROG>
 A:Cross-references: GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987
 A:Experimental source: V. Himalaya
 R:Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B.
 FEBS Lett. 363, 289-303, 1995
 A:Title: Isozyme hydrolase within the protruding third loop domain of the barley alpha-
 A:Reference number: S65602; MUID:95253567; PMID:7737421
 A:Accession: S65602
 A:Molecule type: protein
 A:Residues: 25-29 <JUG>
 A:Comment: Production of this enzyme in barley is hormonally regulated. Germinating b

C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: calcium binding; glycosidase; hydrolase; monomer; polysaccharide degradat
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-438/Product: alpha-amylase #status predicted <AMT>
 F:171-318/Domain: alpha-amylase core homology <AMY>
 F:204,229,315/Active site: Asp, Glu, Asp #status experimental

Query Match 72.1%; Score 44; DB 1; Length 438;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRDDRPYADG 10
 149 CRDDRPYDGS 158

RESULT 6

alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-OSg2) - rice
 S10013
 C:Species: Oryza sativa (rice)
 C:Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R:Huang, N.; Sutcliffe, T.D.; Lites, J.C.; Rodriguez, R.L.
 Plant Mol Biol. 14, 655-668, 1990
 A:Title: Classification and characterization of the rice alpha-amylase multigene faml

A:Reference number: S10013; MUID:91346657; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HUG>
 A:Cross-references: EMBL:X16509; NID:920166; PIDN:CAA34516.1; PID:920167
 A:Experimental source: var. M202
 C:Genetics:
 A:Introns: 30/3; 75/1; 345/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMT>

Query Match
 Best Local Similarity 68.0%; Score 41.5; DB 2; Length 428;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
 |||||
 Db 149 CRDD-PYGDG 157

RESULT 7
 S12775
 alpha-amylase (EC 3.2.1.1) precursor (clone POS103) - rice
 C:Species: Oryza sativa (rice)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: S12775
 R:O'Neill, S.D.; Kungagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and m
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12775
 A:Molecule type: mRNA
 A:Residues: 1-434 <ONE>
 A:Cross-references: EMBL:M24286; NID:9169752; PIDN:AAA33885.1; PID:9169753
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:176-323/Domain: alpha-amylase core homology <AMT>
 F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match
 Best Local Similarity 68.0%; Score 41.5; DB 2; Length 434;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRDDRPYADG 10
 |||||
 Db 155 CRDD-PYGDG 163

RESULT 8
 S04123
 hypothetical protein 151 - Rhizobium meliloti
 C:Species: Rhizobium meliloti
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Oct-1999
 C:Accession: S04123; S32840; S39987
 R:Batut, J.; Davearan-Mingot, M.L.; David, M.; Jacobs, J.; Garnerone, A.M.; Kahn, D.
 EMBO J. 8, 1279-1286, 1989
 A:Title: fixK, a gene homologous with fixr and crp from Escherichia coli, regulates nitro
 A:Reference number: S04122; MUID:89305532; PMID:2663474
 A:Accession: S04123
 A:Molecule type: DNA
 A:Residues: 1-151 <BAT>
 A:Cross-references: EMBL:X15079; NID:948690; PIDN:CAA33184.1; PID:948692
 R:Kahn, D.D.
 submitted to the EMBL Data Library, March 1993
 A:Reference number: S32837
 A:Accession: S32840

A:Molecule type: DNA
 A:Residues: 1-151 <KAH>
 A:Cross-references: EMBL:Z21854; NID:949403; PIDN:CAA79900.1; PID:949407

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 151;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPY 7
 |||||
 Db 26 CRDDPY 32

RESULT 9
 B95345
 hypothetical protein Sma1223 [imported] - Sinorhizobium meliloti (strain 1021) magap1
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: B95345
 R:Barneit, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
 .; Kalman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
 .; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: B95345
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-151 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65324.1; PID:914523781; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hub
 pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma1223
 A:Genome: plasmid

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 151;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CRDDRPY 7
 |||||
 Db 26 CRDDPY 32

RESULT 10
 T03440
 probable chitinase (EC 3.2.1.14) - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
 C:Accession: T03440
 R:Yun, C.H.; Lee, M.C.; Lee, J.S.; Yun, K.J.; Eun, M.Y.
 submitted to the EMBL Data Library, April 1997
 A:Description: isolation and characterization of a rice chitinase cDNA clone from ric
 A:Reference number: Z14947
 A:Accession: T03440
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-278 <YUN>
 A:Cross-references: EMBL:AF001501; NID:92109456; PID:92109457
 A:Experimental source: cv. IR36
 C:Superfamily: plant chitinase; plant chitinase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:54-276/Domain: plant chitinase homology <PCH>

Query Match
 Best Local Similarity 67.2%; Score 41; DB 2; Length 278;

Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDPRPADG 10
|||||
DB 269 CRDCKPYGCG 278

RESULT 11

T09942

alpha-amylase (EC 3.2.1.1) precursor - southern Asian dodder (fragment)

N:Alternate names: alpha-1,4-glucan-4-glucanohydrolase

C:Species: Cuscuta reflexa (southern Asian dodder)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000

C:Accession: T09942

R:Ramachandiran, S.; Srinivasa, B.; Mahadevan, S.

Submitted to the EMBL Data Library, February 1994

A:Description: Molecular cloning and nucleotide sequence of detachment induced alpha amy

A:Reference number: 216900

A:Accession: T09942

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: EMBL:U06754; NID:g458455; PID:g458456

A:Residues: 1-423 <RAM>

C:Genetics:

A:Gene: AMY2

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:165-309/Domain: alpha-amylase core homology <AMY>

Query Match

Best Local Similarity 60.0%; Pred. No. 6.6;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRPADG 10
|||||
DB 143 CRDPTQISDG 152

RESULT 12

T24216

Chromosome condensation protein homolog Dpy-27 - Caenorhabditis elegans

N:Alternate names: protein R13G10.1

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000

C:Accession: T24216; A55095

R:Gardner, A.

submitted to the EMBL Data Library, August 1994

A:Reference number: 219857

A:Accession: T24216

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1469 <NTL>

A:Cross-references: EMBL:Z35602; PIDN:CAA84669.1; GSPDB:GN00021; CESP:R13G10.1

A:Experimental source: clone R13G10

R:Chuang, P.T.; Albertson, D.C.; Meyer, B.J.

Cell 79, 459-474, 1994

A:Title: Dpy-27: a chromosome condensation protein homolog that regulates Caenorhabditis

A:Reference number: A55095; MUID:95042743; PMID:7954812

A:Accession: A55095

A:Status: Preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-1132; GC, 1134-1469 <CHD>

A:Cross-references: GB:J35274; NID:9529384; PIDN:AAA62047.1; PID:9529385

A:Note: authors translated the codon GAT for residue 1133 as GAT

C:Genetics:

A:Gene: CESP:R13G10.1

A:Map position: 3

A:Introns: 142/3; 176/3; 296/2; 548/2; 627/3; 697/2; 847/3; 993/3; 1086/2; 1202/3; 1383/

C:Superfamily: chromosome segregation protein SMC1

Query Match 67.2%; Score 41; DB 2; Length 1469;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDRPYAD 9
|||||
DB 13 DDRPYAD 19

RESULT 13

AE0281

Two-component regulatory system, response regulator protein rsta [Imported] - Yersinia

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001

C:Accession: AE0281

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AE0281

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-248 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC91113.1; PID:g15980304; GSPDB:GN00175

C:Genetics:

A:Gene: rsta

C:Superfamily: ompr protein; response regulator homology

Query Match

Best Local Similarity 70.0%; Pred. No. 6;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRPADG 10
|||||
DB 64 CRDPRPADG 73

RESULT 14

JQ1527

alpha-amylase (EC 3.2.1.1) 2A - rice

C:Species: Oryza sativa (rice)

C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999

C:Accession: JQ1527

R:Huang, N.; Reihl, S.J.; Rodriguez, R.L.

Gene 111, 223-228, 1992

A:Title: Rany2A: a novel alpha-amylase-encoding gene in rice.

A:Reference number: JQ1527; MUID:92175526; PMID:1541400

A:Accession: JQ1527

A:Molecule type: DNA

A:Residues: 1-443 <HUA>

A:Cross-references: GB:M74177; NID:g169768; PIDN:AAA33894.1; PID:g169769

C:Comment: Rice alpha-amylases are encoded by three multigene families, Amy1, Amy2

C:Genetics:

A:Gene: RANY2A

A:Introns: 27/3; 71/2; 345/3

C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: wheat alpha-amylase; alpha-amylase core homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:108-31/Domain: alpha-amylase core homology <AMY>

F:202,220,314/Active site: Asp, Glu, Asp status predicted

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 443;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRPADG 10
|||||
DB 146 CRDPTQISDG 155

RESULT 15
 S19990
 alpha-amylase (EC 3.2.1.1) - rice
 C:Species: Oryza sativa (rice)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S19990
 R:Goldman, S.; Mawal, Y.; Wu, R.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S19990
 A:Accession: S19990
 A:Molecule type: mRNA
 A:Residues: 1-445 <GOL>
 A:Cross-references: EMBL:X64619; NID:g20172; PIDN:CAA45903.1; PID:g20173
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:168-317/domain: alpha-amylase core homology <AMY>
 F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 65.6%; Score 40; DB 2; Length 445;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDPYADG 10
 |||||
 Db 146 CRDDPYFSDG 155

RESULT 16
 H70971
 hypothetical protein RV3369 - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: H70971
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garner, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:96295987; PMID:9634230
 A:Accession: H70971
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-144 <COL>
 A:Cross-references: GB:AL009198; GB:AL123456; NID:g3242262; PIDN:CAA15754.1; PID:g266164
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3369
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV3369

Query Match 63.9%; Score 39; DB 2; Length 144;
 Best Local Similarity 85.7%; Pred. No. 5.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDDPY 7
 |||||
 Db 101 CRDDPY 107

RESULT 17
 A87358
 hypothetical protein CC0876 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: A87358
 R:Nierman, W.C.; Felblylun, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.C.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87358
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1370 <STO>
 A:Cross-references: GB:A8005673; NID:g13422137; PIDN:AAK22861.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC0876

Query Match 63.9%; Score 39; DB 2; Length 370;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RDDRPRADG 10
 |||||
 Db 234 RDDRPRADG 242

RESULT 18
 AB2711
 30S ribosomal protein S6 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C:Species: *Agrobacterium tumefaciens*
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AB2711
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chan, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl, science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
 A:Title: The genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AB2711
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1153 <KUR>
 A:Cross-references: GB:A8008688; PIDN:AAK42104.1; PID:g17739486; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: rpsF
 A:Map position: circular chromosome
 C:Superfamily: *Escherichia coli* ribosomal protein S6

Query Match 62.3%; Score 38; DB 2; Length 153;
 Best Local Similarity 77.8%; Pred. No. 8.8;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RDDRPRADG 10
 |||||
 Db 109 RDDRPRADG 117

RESULT 19
 J01648
 SHL2 protein - human herpesvirus 6
 C:Species: human herpesvirus 6
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
 C:Accession: J01648
 R:Efsthliou, S.; Lawrence, G.L.; Brown, C.M.; Barrell, B.G.
 J. Gen. Virol. 73, 1661-1671, 1992
 A:Title: Identification of homologues to the human cytomegalovirus US22 gene family 1
 A:Reference number: J01647; MUID:92333249; PMID:1321206
 A:Accession: J01648
 A:Molecule type: DNA
 A:Residues: 1-373 <EPS>
 A:Cross-references: DDBJ:D10082; NID:g221456; PIDN:BAA00977.1; PID:g221458
 A:Experimental source: strain UI102
 C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 373;
 Best Local Similarity 66.7%; Pred. No. 21;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CRDPRVAD 9
 |||: |||
 DB 90 CRDENEYAD 98

RESULT 20
 T43962
 hypothetical protein U3 [imported] - human herpesvirus 6 (strain HST)
 C:Species: human herpesvirus 6
 A:Variety: strain HST
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T43962
 R:Issigawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
 J. Virol. 73, 8053-8063, 1999
 A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
 A:Reference number: 222732; MUID:99412319; PMID:10482554
 A:Accession: T43962
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1386 <1386>
 A:Cross-references: EMBL:AB021506; NID:g4995977; PIDN:BAV8223.1; PID:g4995990
 A:Experimental source: strain HST; pop. variant B
 C:Genetics:
 A:Note: U3
 C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 386;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CRDPRVAD 9
 |||: |||
 DB 103 CRDENEYAD 111

RESULT 21
 T44151
 hypothetical protein U3 [imported] - human herpesvirus 6 (strain Z29)
 C:Species: human herpesvirus 6
 A:Variety: strain Z29
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Jun-2000
 C:Accession: T44151
 R:Domineq, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
 J. Virol. 73, 8040-8052, 1999
 A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
 A:Reference number: 222734; MUID:99412318; PMID:10482553
 A:Accession: T44151
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1386 <DOM>
 A:Cross-references: EMBL:AF157706; PIDN:ADA9622.1
 A:Experimental source: strain Z29; variant B
 C:Genetics:
 A:Note: U3
 C:Superfamily: human herpesvirus 6 SHL2 protein

Query Match 62.3%; Score 38; DB 2; Length 386;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CRDPRVAD 9
 |||: |||
 DB 103 CRDENEYAD 111

RESULT 22
 S12625
 alpha-amylase (EC 3.2.1.1) 3D - rice
 C:Species: Oryza sativa (rice)
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 22-Jun-1999
 C:Accession: S12625; S12776; S15054; J10945

R: Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
 Nucleic Acids Res. 18, 7007-7014, 1990
 A:Title: Structural organization and differential expression of rice alpha-amylase ge
 A:Reference number: J10945; MUID:91088278; PMID:2263460
 A:Accession: S12625
 A:Molecule type: DNA
 A:Residues: 1-435 <HUA>

A:Cross-references: EMBL:M59351; NID:9169770; PIDN:AAA3895.1; PID:9169771
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12776
 A:Molecule type: mRNA
 A:Residues: 1-435 <ONE>
 A:Cross-references: EMBL:M24287
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R L
 submitted to the EMBL Data Library April 1989
 A:Description: The alpha-amylase genes in Oryza sativa: Characterization of cDNA clon
 A:Reference number: S15054
 A:Accession: S15054
 A:Molecule type: mRNA
 A:Residues: 1-72, 'R', 75-136, 'R', 138-435 <ON2>
 A:Cross-references: EMBL:M24287; NID:9169754; PIDN:AAA3886.1; PID:9169755
 C:Genetics:
 A:Insertions: 30/3; 342/3
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-314/Domain: alpha-amylase core homology <AMY>
 F:203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 62.3%; Score 38; DB 2; Length 435;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 CRDPRVAD 10
 |||: |||
 DB 148 CSDPTQYSDS 157

RESULT 23
 S71804
 receptor-like serpentine protein smoothened - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
 C:Accession: S71804
 R:van den Heuvel, M.; Ingham, P.W.
 Nature 382, 547-551, 1996
 A:Title: smoothened encodes a receptor-like serpentine protein required for hedgehog
 A:Reference number: S71804; MUID:96320560; PMID:8700230
 A:Accession: S71804
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-1024 <VAN>
 A:Note: Intron-exon boundaries were confirmed by sequencing fragments of the genomic

Query Match 62.3%; Score 38; DB 2; Length 1024;
 Best Local Similarity 66.7%; Pred. No. 158;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 RDDRPRVAD 10
 |||: |||
 DB 56 RDDKPRWFDG 64

RESULT 24
 A26311
 nerve growth factor beta chain precursor - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 21-Jul-2000

C:Accession: A26311; A24857; S00127; S12532
 R:Ebdendal, T.; Larhammar, D.; Persson, H.
 EMBO J. 5, 1483-1487, 1986
 A:Title: Structure and expression of the chicken beta nerve growth factor gene.
 A:Reference number: A26311; MUID:86300646; PMID:3017695
 A:Accession: A26311
 A:Molecule type: mRNA
 A:Residues: 1-243 <EBE>
 A:Cross-references: GB:X04003; NID:963697; PIDN:CAA27633.1; PID:g1334740
 R:Wion, D.; Perret, C.; Frechin, N.; Keller, A.; Behar, G.; Brachet, P.; Auffray, C.
 FEBS Lett. 203, 82-86, 1986
 A:Title: Molecular cloning of the avian beta-nerve growth factor gene: transcription in
 A:Reference number: A24857; MUID:86248129; PMID:3720959
 A:Accession: A24857
 A:Molecule type: DNA
 A:Residues: 118-243 <MIO>
 A:Cross-references: GB:D00010; GB:N00010; GB:X04067; NID:9222840; PIDN:BA000008.1; PID:g
 R:Meier, R.; Becker-Andre, M.; Goetz, R.; Heumann, R.; Shaw, A.; Thoenen, H.
 EMBO J. 5, 1489-1493, 1986
 A:Title: Molecular cloning of bovine and chick nerve growth factor (NGF): delineation of
 A:Reference number: A26312; MUID:86300647; PMID:2427334
 A:Accession: S00127
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 121-243 <MET>
 A:Cross-references: GB:M26810; NID:g212446; PIDN:AAA48984.1; PID:g212447
 R:Ibanez, C.F.; Halboeck, F.; Ebdendal, T.; Persson, H.
 EMBO J. 9, 1477-1483, 1990
 A:Title: Structure-function studies of nerve growth factor: functional importance of hig
 A:Reference number: S12532; MUID:90228346; PMID:2338722
 A:Accession: S12532
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 126-243 <IBA>
 A:Superfamily: nerve growth factor beta chain
 C:Keywords: growth factor
 F:1-125/Domain: signal sequence #status predicted <SIG>
 F:126-243/Product: nerve growth factor beta chain #status predicted <MAT>
 Query Match 60.7%; Score 37; DB 2; Length 243;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 CRDPRYADG 10
 Db 182 CRDPRVSSG 191
 RESULT 25
 C47031 of bah - Streptomyces hygroscopicus
 C:Species: Streptomyces hygroscopicus
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: C47031
 R:Raibaud, A.; Zalacain, M.; Holt, T.G.; Tizard, R.; Thompson, C.J.
 J. Bacteriol. 173, 4454-4463, 1991
 A:Title: Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase, t
 A:Reference number: A47031; MUID:91294191; PMID:2066341
 A:Accession: C47031
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-253 <RAI>
 A:Cross-references: GB:M64783; NID:g153172; PIDN:AAA9278.1; PID:g153174
 A:Note: sequence extracted from NCBI backbone (NCBIN:41300, NCBI:41305)
 C:Superfamily: oleoyl-[acyl-carrier-protein] hydrolase; oleoyl-[acyl-carrier-protein] hy
 F:16-228/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>
 Query Match 60.7%; Score 37; DB 1; Length 253;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 RDDRPRYADG 10

Db 124 KTERPYGDG 132
 RESULT 26
 T11610
 C:Species: Vigna unguiculata (cowpea)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T11610
 R:Juch, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Terao, T.; Shinozaki, K.
 Plant Cell Physiol. 37, 1073-1082, 1996
 A:Title: Novel drought-inducible genes in the highly drought-tolerant cowpea:cloning
 A:Reference number: Z17294; MUID:97185229; PMID:9032963
 A:Accession: T11610
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-325 <UGC>
 A:Cross-references: EMBL:D83971; NID:g1854444; PIDN:BA012161.1; PID:g1854445
 A:Experimental source: strain IT84S-2246-4
 C:Superfamily: dihydrokaempferol 4-reductase
 C:Keywords: oxidoreductase
 Query Match 60.7%; Score 37; DB 2; Length 325;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CRDPRY 7
 Db 279 CVDDRPY 285
 RESULT 27
 T29442
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002
 C:Accession: T29442
 R:Blanchard, M.; Bradshaw, H.
 submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid F08F3.
 A:Reference number: Z20620
 A:Accession: T29442
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-463 <BLA>
 A:Cross-references: EMBL:U64847; PIDN:AA04874.1; GSPDB:GN00023; CESP:F08F3.3
 A:Experimental source: strain Bristol N2; clone F08F3
 C:Genetics:
 A:Gene: CESP:F08F3.3
 A:Map position: 5
 A:Inserts: 18/3; 167/3; 266/3; 362/2; 442/3
 C:Superfamily: human erythrocyte membrane protein Rhd
 Query Match 60.7%; Score 37; DB 2; Length 463;
 Best Local Similarity 77.8%; Pred. No. 41;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 RDDRPRYADG 10
 Db 420 RDDRPRYADG 428
 RESULT 28
 F87317
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: F87317
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87317
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1521<SNO>
A:Cross-references: GB:A005673; NID:g13421742; PIDN:AAK22538.1; GSPDB:GN00148
C:Genetic: CC0551
A:Gene: CC0551

Query Match 60.7%; Score 37; DB 2; Length 521;
Best Local Similarity 85.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RODRPA 8
Db 107 RODRPA 113

RESULT 29

S71008
propionyl-CoA carboxylase beta chain homolog - *Saccharopolyspora erythraea*
C:Species: *Saccharopolyspora erythraea*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S71008
R:Donadio, S.; Staver, M.J.; Katz, L.
Mol. Microbiol. 19, 977-984, 1996
A:Title: Erythromycin production in *Saccharopolyspora erythraea* does not require a function
A:Reference number: S71005; MUID:96249691; PMID:8830278
A:Accession: S71008
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-546<DON>
A:Cross-references: EMBL:X92557; NID:g1177651; PIDN:CAA63310.1; PID:g1177652
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: pccB
C:Superfamily: propionyl-CoA carboxylase beta chain

Query Match 60.7%; Score 37; DB 1; Length 546;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DRPYADG 10
Db 87 DRPYDG 93

RESULT 30

C84976
tRNA (guanine-N1)-methyltransferase (EC 2.1.1.31) [imported] - *Buchnera* sp. (strain Aps
C:Species: *Buchnera* sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: C84976
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. A
A:Reference number: A84930; MUID:2045173; PMID:10993077
A:Accession: C84976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237<SNO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain Aps
C:Genetics:
A:Gene: tmd; BU396
C:Superfamily: tRNA (guanine-N1) methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 59.0%; Score 36; DB 2; Length 237;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DRPYADG 10
Db 59 DRPYGCG 66

Search completed: August 29, 2003, 18:48:29
Job time: 11.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:39:11 ; Search time 6.57143 Seconds

(without alignments)
71.562 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDPRYADG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 61 | 100.0 | 368 | 1 | AMY3_HORVU |
| 2 | 61 | 100.0 | 427 | 1 | AMY2_HORVU |
| 3 | 56 | 91.8 | 429 | 1 | AMY6_HORVU |
| 4 | 44 | 72.1 | 421 | 1 | AMYA_VIGMU |
| 5 | 44 | 72.1 | 438 | 1 | AMY1_HORVU |
| 6 | 41.5 | 68.0 | 428 | 1 | AMY1_ORYSA |
| 7 | 41 | 67.2 | 151 | 1 | Y4G6_RHIME |
| 8 | 41 | 67.2 | 1469 | 1 | DP27_CAEEL |
| 9 | 40 | 65.6 | 445 | 1 | AMY2_ORYSA |
| 10 | 40 | 65.6 | 443 | 1 | AMY2_ORYSA |
| 11 | 38 | 62.3 | 149 | 1 | RS6_RHIME |
| 12 | 38 | 62.3 | 373 | 1 | VU3_HSV6U |
| 13 | 38 | 62.3 | 435 | 1 | AMY3_ORYSA |
| 14 | 38 | 62.3 | 1036 | 1 | SMO_DROME |
| 15 | 38 | 62.3 | 3255 | 1 | POIG_LMVE |
| 16 | 37 | 60.7 | 243 | 1 | NGF_CHICK |
| 17 | 37 | 60.7 | 546 | 1 | PCCR_SACBR |
| 18 | 37 | 60.7 | 519 | 1 | IRX4_HUMAN |
| 19 | 36.5 | 59.8 | 237 | 1 | TRMD_BUCAL |
| 20 | 36 | 59.0 | 245 | 1 | TRMD_HASN1 |
| 21 | 36 | 59.0 | 246 | 1 | TRMD_HASN1 |
| 22 | 36 | 59.0 | 246 | 1 | TRMD_VIBR8 |
| 23 | 36 | 59.0 | 249 | 1 | TRMD_VIBR8 |
| 24 | 36 | 59.0 | 250 | 1 | TRMD_BUCP |
| 25 | 36 | 59.0 | 255 | 1 | TRMD_ECOLI |
| 26 | 36 | 59.0 | 255 | 1 | TRMD_ECOLI |
| 27 | 36 | 59.0 | 255 | 1 | TRMD_SALTI |
| 28 | 36 | 59.0 | 255 | 1 | TRMD_SALTY |
| 29 | 36 | 59.0 | 255 | 1 | TRMD_SERNA |
| 30 | 36 | 59.0 | 262 | 1 | TRMD_BUCAP |
| 31 | 36 | 59.0 | 262 | 1 | TRMD_RALSO |
| 32 | 36 | 59.0 | 423 | 1 | YW2_CAEEL |
| 33 | 36 | 59.0 | 440 | 1 | AMY3_ORYSA |

| | | | | | | |
|-----|------|------|------|---|------------|---------------------|
| 34 | 36 | 59.0 | 539 | 1 | Y4Q1_RHISN | P55630 rhizobium s |
| 35 | 35 | 57.4 | 85 | 1 | YPB5_BACSU | P54160 bacillus su |
| 36 | 35 | 57.4 | 165 | 1 | UBC7_YEAST | Q02159 saccharomyc |
| 37 | 35 | 57.4 | 226 | 1 | NEUM_RAT | P07936 rattus norv |
| 38 | 35 | 57.4 | 227 | 1 | NEUM_MOUSE | P06837 mus musculu |
| 39 | 35 | 57.4 | 659 | 1 | VE1_HP03 | P36719 human papil |
| 40 | 35 | 57.4 | 660 | 1 | VE1_HP03 | P50764 human papil |
| 41 | 35 | 57.4 | 662 | 1 | VE1_HP03 | P50763 human papil |
| 42 | 34 | 55.7 | 197 | 1 | HANI_XENLA | Q73615 xenopus lae |
| 43 | 34 | 55.7 | 231 | 1 | NGF_XENLA | P21617 xenopus lae |
| 44 | 34 | 55.7 | 276 | 1 | METG_PASMU | Q9CK95 pasteurella |
| 45 | 34 | 55.7 | 309 | 1 | MOTB_PASMU | P550108 saccharomyc |
| 46 | 34 | 55.7 | 393 | 1 | MOTB_PASMU | Q8EYCT methanopyru |
| 47 | 34 | 55.7 | 535 | 1 | YKX_HALNI | Q8HND4 anabaena sp |
| 48 | 34 | 55.7 | 548 | 1 | YKX_HALNI | Q8HND4 halobacteri |
| 49 | 34 | 55.7 | 554 | 1 | YKX_HALNI | Q8HND4 halobacteri |
| 50 | 34 | 55.7 | 704 | 1 | GYR2_YEAST | P27472 saccharomyc |
| 51 | 34 | 55.7 | 759 | 1 | METE_MYCLE | Q05564 mycobacteri |
| 52 | 34 | 55.7 | 760 | 1 | METE_MYCLE | Q05564 mycobacteri |
| 53 | 34 | 55.7 | 1310 | 1 | CPA4_MOUSE | Q09647 mus musculu |
| 54 | 34 | 55.7 | 1433 | 1 | REST_CHICK | Q42184 gallus gall |
| 55 | 33 | 54.1 | 200 | 1 | RS4_CAMEL | P59130 oenobacill |
| 56 | 33 | 54.1 | 208 | 1 | RS4_CAMEL | Q09681 campylobact |
| 57 | 33 | 54.1 | 216 | 1 | RNP1_HUMAN | Q09029 homo sapien |
| 58 | 33 | 54.1 | 237 | 1 | RNP1_MOUSE | Q62176 mus musculu |
| 59 | 33 | 54.1 | 247 | 1 | TRMD_VIBR8 | Q9KUF8 vibrio chol |
| 60 | 33 | 54.1 | 308 | 1 | MOTB_ECOLI | P08349 escherichia |
| 61 | 33 | 54.1 | 319 | 1 | YKX_HALNI | Q83852 treponema p |
| 62 | 33 | 54.1 | 319 | 1 | YKX_HALNI | P38803 saccharomyc |
| 63 | 33 | 54.1 | 334 | 1 | YKX_HALNI | P14358 frog vitru |
| 64 | 33 | 54.1 | 394 | 1 | YKX_HALNI | P08117 triticum ae |
| 65 | 33 | 54.1 | 413 | 1 | AMY3_WHEAT | P27939 oryza sativ |
| 66 | 33 | 54.1 | 437 | 1 | AMY3_ORYSA | P27934 oryza sativ |
| 67 | 33 | 54.1 | 437 | 1 | AMY3_ORYSA | P27937 oryza sativ |
| 68 | 33 | 54.1 | 438 | 1 | AMY3_ORYSA | Q50591 mycobacteri |
| 69 | 33 | 54.1 | 479 | 1 | YKX_HALNI | Q50591 mycobacteri |
| 70 | 33 | 54.1 | 574 | 1 | YKX_HALNI | Q50591 mycobacteri |
| 71 | 33 | 54.1 | 578 | 1 | YKX_HALNI | Q50591 mycobacteri |
| 72 | 33 | 54.1 | 772 | 1 | DEG1_CAMEL | P24585 caenorhabdi |
| 73 | 33 | 54.1 | 778 | 1 | LI00_ADEP3 | Q9YER7 porcine ade |
| 74 | 33 | 54.1 | 919 | 1 | AMY_STRLI | Q05684 streptomyce |
| 75 | 33 | 54.1 | 960 | 1 | CAP2_MESCR | P16097 mesembryant |
| 76 | 33 | 54.1 | 964 | 1 | CAP1_TOBAC | P27154 nicotiana t |
| 77 | 33 | 54.1 | 966 | 1 | CAP1_MESCR | P10490 mesembryant |
| 78 | 33 | 54.1 | 967 | 1 | CAP1_MESCR | Q96670 arabidopsis |
| 79 | 33 | 54.1 | 997 | 1 | ATV2_CAMEL | Q46674 c sarcoplas |
| 80 | 33 | 54.1 | 997 | 1 | ATV2_CAMEL | Q00779 f sarcoplas |
| 81 | 33 | 54.1 | 998 | 1 | RRPO_BOOLV | Q09270 boolaria vi |
| 82 | 33 | 54.1 | 1044 | 1 | ATV2_CAMEL | Q55143 m sarcoplas |
| 83 | 32.5 | 53.3 | 122 | 1 | YKX_HALNI | P76001 escherichia |
| 84 | 32.5 | 53.3 | 515 | 1 | YKX_HALNI | Q96751 mus musculu |
| 85 | 32 | 52.5 | 98 | 1 | YKX_HALNI | Q63751 rattus norv |
| 86 | 32 | 52.5 | 135 | 1 | YKX_HALNI | Q27030 methanobact |
| 87 | 32 | 52.5 | 155 | 1 | YKX_HALNI | P24836 human papil |
| 88 | 32 | 52.5 | 202 | 1 | YKX_HALNI | P05452 homo sapien |
| 89 | 32 | 52.5 | 202 | 1 | YKX_HALNI | P43025 mus musculu |
| 90 | 32 | 52.5 | 209 | 1 | YKX_HALNI | Q9X113 thermotoga |
| 91 | 32 | 52.5 | 218 | 1 | YKX_HALNI | Q10334 oryza pseu |
| 92 | 32 | 52.5 | 249 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 93 | 32 | 52.5 | 249 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 94 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 95 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 96 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 97 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 98 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 99 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |
| 100 | 32 | 52.5 | 252 | 1 | YKX_HALNI | Q9J410 neisseria m |

ALIGNMENTS

RESULT 1

AMY2_HORVU STANDARD; PRT; 368 AA.

AC P04063;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY1.2) (High pi alpha-amylase).
 GN AMY1.2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chandra G.R., Huang J.K., Clark K.L., Reeck G.R.,
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley."
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chandra G.R., Huang J.K., Clark K.L., Reeck G.R.,
 RT "Two barley alpha-amylase gene families are regulated differently in aleurone cells."
 RL J. Biol. Chem. 260:3731-3738(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RA MEDLINE=94254083; PubMed=8196040;
 RX Kadziola A., Abe J.-I., Svensson B., Haser R.;
 RT "Crystal and molecular structure of barley alpha-amylase."
 RL J. Mol. Biol. 239:104-121(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
 RC STRAIN-CV. Mennet;
 RX MEDLINE=98298441; PubMed=9634702;
 RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
 RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9-A resolution."
 RL Structure 6:649-659(1998).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- CORFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC -----
 DR EMBL; K02633; JAAV.
 DR HSSP; P04063; JAAV.
 DR InterPro: IPR006589; Alp_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 203 203 BY SIMILARITY.
 FT ACT_SITE 228 228 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT NON_TER 368 368
 FT SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;
 Query Match 100.0%; Score 61; DB 1; Length 368;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AMY2_HORVU STANDARD; PRT; 427 AA.

AC P04063;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pi alpha-amylase).
 GN AMY2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rahmatullah R.J., Huang J.K., Clark K.L., Reeck G.R.,
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pi alpha-amylases from barley."
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chandra G.R., Huang J.K., Clark K.L., Reeck G.R.,
 RT "Two barley alpha-amylase gene families are regulated differently in aleurone cells."
 RL J. Biol. Chem. 260:3731-3738(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RA MEDLINE=94254083; PubMed=8196040;
 RX Kadziola A., Abe J.-I., Svensson B., Haser R.;
 RT "Crystal and molecular structure of barley alpha-amylase."
 RL J. Mol. Biol. 239:104-121(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
 RC STRAIN-CV. Mennet;
 RX MEDLINE=98298441; PubMed=9634702;
 RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
 RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9-A resolution."
 RL Structure 6:649-659(1998).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- CORFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- INDUCTION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC -----
 DR EMBL; X15226; CAA33298.1; -
 DR EMBL; K02637; AAA98790.1; -
 DR PIR; A31960; ALBHB.
 DR PDB; 1AMV; 13-MAY-95.
 DR PDB; 1AVA; 16-MAR-99.
 DR PDB; 1BG9; 15-JUN-99.

RESULT 2
 AMY2_HORVU

DR InterPro: IPR006589; Alp_amiL_cat.sub.
 DR InterPro: IPR006047; Alpha_amiL_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PR00128; alpha-amyase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KM Hydrolyase; glycosidase; Carbohydrate metabolism; Seed; Germination;
 KM Calcium; Multigene family; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 427
 FT ACT_SITE 203 203
 FT ACT_SITE 228 228
 FT ACT_SITE 313 313
 FT ACT_SITE 134 134
 FT CONFLICT 195 197
 FT CONFLICT 425 425
 FT CONFLICT 27 29
 FT STRAND 33 34
 FT TURN 35 37
 FT HELIX 39 40
 FT HELIX 42 47
 FT TURN 48 49
 FT HELIX 50 56
 FT TURN 57 57
 FT STRAND 60 63
 FT TURN 69 69
 FT TURN 72 73
 FT STRAND 77 77
 FT TURN 80 81
 FT TURN 84 85
 FT TURN 87 88
 FT HELIX 91 104
 FT TURN 105 105
 FT STRAND 107 112
 FT STRAND 116 116
 FT STRAND 121 122
 FT TURN 124 125
 FT STRAND 128 130
 FT TURN 139 140
 FT HELIX 144 146
 FT STRAND 147 147
 FT TURN 149 150
 FT TURN 152 154
 FT STRAND 155 165
 FT TURN 168 169
 FT STRAND 172 173
 FT TURN 175 176
 FT HELIX 178 193
 FT TURN 194 195
 FT STRAND 199 202
 FT TURN 203 204
 FT HELIX 205 207
 FT TURN 210 220
 FT STRAND 224 227
 FT TURN 235 235
 FT STRAND 237 238
 FT TURN 241 241
 FT HELIX 246 260
 FT TURN 261 262
 FT STRAND 265 268
 FT HELIX 270 279
 FT TURN 280 282
 FT HELIX 284 287
 FT TURN 290 291
 FT TURN 297 299
 FT HELIX 300 300
 FT TURN 302 304
 FT STRAND 305 308
 FT TURN 312 314
 FT TURN 316 318
 FT HELIX 325 327
 FT HELIX 328 337
 FT STRAND 341 345

ALPHA-AMYLASE TYPE B ISOZYME.
 G -> D (IN REF. 1).
 IGF -> HRL (IN REF. 2).
 E -> Q (IN REF. 1).

FT HELIX 346 350
 FT TURN 351 351
 FT HELIX 355 357
 FT TURN 368 369
 FT TURN 372 373
 FT STRAND 376 382
 FT TURN 383 384
 FT STRAND 385 390
 FT TURN 391 393
 FT STRAND 394 398
 FT HELIX 405 407
 FT STRAND 412 418
 FT TURN 419 420
 FT STRAND 421 427
 SQ SEQUENCE 427 AA; 47355 MW; 957C0B16621BF748 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 427;
 Best local similarity 100.0%; Pred. No. 0.00092;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDREYADG 10
 |||||
 Db 148 CRDDREYADG 157

RESULT 3
 ANY6_HORVU STANDARD: PRT: 429 AA.
 AC P04750.
 DT 13-AUG-1987 (Rel. 05; Created)
 DT 01-NOV-1980 (Rel. 16; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE Alpha-amyase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase) (Clones GRAM56 and 963).
 GN AMYL.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A. (CLONE GRAM56).
 RA Rahmatullah R.J., Huang J.-K., Clark K.L., Reeck G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes
 RT for high-pI alpha-amyases from barley."
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE OF 380-429 FROM N.A. (CLONE 963).
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Seegle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amyase gene family in barley
 RT aleurones."
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
 CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
 CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING
 CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
 CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
 CC DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED
 CC CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH
 CC GIBBERELLIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC EMBL: X15227; CAA33229.1; -
 DR EMBL: K02636; AAA32932.1; -
 DR PIR: J0406; J0406.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; ALP_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 47937 MW; 1C924CA6319D5262 CRC64;

Query Match 91.8%; Score 56; DB 1; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.0075;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
 Db 148 CRDDRPYDGD 157
 |||||
 |||||

RESULT 4
 AMYA_VIGMU STANDARD; PRT; 421 AA.
 AC P17859;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.1.
 OS Vigna mungo (Rice bean) (Black gram).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 CC NCBI_TaxID=3913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cotyledon;
 RX MEDLINE=90332425; PubMed=2377468;
 RA Yamauchi D., Minamikawa T.;
 RT "Nucleotide sequence of cDNA for alpha-amy1ase from cotyledons of
 RT germinating Vigna mungo seeds.";
 RL Nucleic Acids Res. 18:4250-4250(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94120017; PubMed=8290640;
 RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
 RT "Nucleotide sequence of the alpha-amy1ase gene from Vigna mungo.";
 RL Plant Physiol. 103:1459-1459(1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC EMBL: X53049; CAA37217.1; -
 DR EMBL: X73301; CAA51734.1; -
 DR PIR: S10514; S10514.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; ALP_amy1_cat_sub.
 DR InterPro: IPR006047; Alpha_amy1_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amy1ase; 1.
 DR PRINTS: PR00110; ALPHAAMYLASE.
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; signal.
 FT SIGNAL 1 23
 FT CHAIN 24 421 PROBABLE.
 FT ACT_SITE 201 201 ALPHA-AMYLASE.
 FT ACT_SITE 309 309 BY SIMILARITY.
 FT METAL 113 113 CALCIUM (BY SIMILARITY).
 FT METAL 172 172 CALCIUM (BY SIMILARITY).
 SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 421;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDRPYADG 10
 Db 146 CRDDTATSDG 155
 |||||
 |||||

RESULT 5
 AMYL_HORVU STANDARD; PRT; 438 AA.
 AC P00653;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amy1ase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
 DE glucan glucanohydrolase) (AMY1) (low pI alpha-amy1ase).
 GN AMY1.1.
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticeae; Hordeum.
 CC NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Himalaya;
 RX MEDLINE=83238423; PubMed=6190808;
 RA Rogers J.C., Millman C.;
 RT "Isolation and sequence analysis of a barley alpha-amy1ase cDNA
 RT clone.";
 RL J. Biol. Chem. 258:8169-8174(1983).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY
 CC REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC
 CC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALBURNONE CELLS COVERING
 CC THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME
 CC THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE
 CC DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC -----
DR EMBL: J01236; AAA3292.1;
DR PIR: A00846; ALBH.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006589; Alp-amy1_cat_sub.
DR InterPro: IPR006047; Alpha-amy1_cat.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR SMART: SM00642; Amy; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family; Signal.
FT SIGNAL
FT CHAIN 1 24
FT ACT_SITE 23 438 ALPHA-AMYLASE TYPE A ISOZYME.
FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 229 229 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
SQ SEQUENCE 438 AA; 47796 MW; 2393FDC5180F51 CRC64;

Query Match 72.1%; Score 44; DB 1; Length 438;
Best Local Similarity 70.0%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDPRPYADG 10
DB 149 CRDPRKYS DG 158

RESULT 6
AMY1_ORYSA STANDARD; PRT: 428 AA.
AC P17654;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Isozyme 1B).
GN AMY1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202;
RX MEDLINE=91346657; PubMed=2102847;
RA Huang N., Sutcliffe T.D., Lites J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amy1ase
RT multigene family."
RL Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS103).
RC STRAIN=cv. Japonica M202;
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutcliffe T.D.,
RA Rodriguez R.L.;
RT "The alpha-amy1ase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Gen. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COPACOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALDUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALCOHOLIC CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PFM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC -----
DR EMBL: X16509; CAA34516.1;
DR EMBL: M24286; AAA33885.1; ALT_INIT.
DR PIR: S10013; S10013.
DR HSSP: P04063; IAVA.
DR Gramene: P17654;
DR InterPro: IPR006589; Alp-amy1_cat_sub.
DR InterPro: IPR006047; Alpha-amy1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Glycoprotein; Multigene family.
FT SIGNAL 1 25 PROBABLE.
FT CHAIN 26 428 ALPHA-AMYLASE.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 116 116 CALCIUM (BY SIMILARITY).
FT METAL 174 174 CALCIUM (BY SIMILARITY).
FT CARBOHYD 265 265 N-LINKED (GLUCNA... ) (PROBABLE).
SQ SEQUENCE 428 AA; 47755 MW; 3B71403ACFC6A6 CRC64;

Query Match 68.0%; Score 41.5; DB 1; Length 428;
Best Local Similarity 80.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRDPRPYADG 10
DB 149 CRDPRPYDG 157

RESULT 7
YAG6_RHIME STANDARD; PRT: 151 AA.
AC P13486;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein RA0666.
GN RA0666 OR SMA1223.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89305532; PubMed=2663474;
RA Bhatt J., Daverin-Mingot M.-L., David M., Jacobs J., Garnerone A.-M.,
RA Kahn D.,
RT "FixX, a gene homologous with fixr and cfp from Escherichia coli,
RT regulates nitrogen fixation genes both positively and negatively in
RT Rhizobium meliloti."
RL EMBO J. 8:1279-1286(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.-J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barlow-Hubler F., Bowser L., Capela D., Gilbert F., Gouzy J.,
RA Gurjal M., Hong A., Hultzer L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kallman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire

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RT Sinorhizobium meliloti pSyma megaplasmid";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
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 CC -----
 DR EMBL: X15079; CAA33184.1; -
 DR EMBL: Z21854; CAA79900.1; -
 DR EMBL: AE007255; AAK65324.1; -
 DR PIR: B95345; B95345;
 DR PIR: S04123; S04123;
 KW Hypothetical protein; Nitrogen fixation; Plasmid; Complete proteome.
 SQ SEQUENCE 151 AA; 17013 MW; C646ED93410F1E09 CRC64;
 Query Match 67.2%; Score 41; DB 1; Length 151;
 Best Local Similarity 85.7%; Pred. No. 1.4;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CRDDRPY 7
 Db 26 CRDDQPY 32
 RESULT 8
 ID DP27_CAEEL STANDARD; PRT; 1469 AA.
 AC PA8996;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Chromosome condensation protein dpy-27 (Dumpy-27 protein).
 GS dpy-27 OR R13G10.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RN SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP IYS-128.
 RC STRAIN-Bristol N2;
 RA Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SUBCELLULAR LOCATION.
 RP MEDLINE=96017644; PubMed=7588066;
 RA Hsu D.R., Chuang P.-T., Meyer B.J.;
 RT "dpy-30, a nuclear protein essential early in embryogenesis for
 RT Caenorhabditis elegans dosage compensation.";
 RL Development 121:3323-3334(1995).
 RN [4]
 RN FUNCTION, AND IDENTIFICATION IN A COMPLEX WITH DPY-26.
 RP MEDLINE=97094383; PubMed=8939870;
 RA Chuang P.-T., Lieb J.D., Meyer B.J.;
 RT "Sex-specific assembly of a dosage compensation complex on the
 RT nematode X chromosome.";
 RL Science 274:1736-1739(1996).
 CC -1- FUNCTION: Involved in X dosage compensation chromosome. Required
 CC to reduce expression of both hermaphrodite X chromosomes. Its
 CC strong similarity with the condensin subunit smc4 suggests that it

CC may reduce the X-chromosome transcript level by condensing the
 CC chromatin structure during interphase cells.
 CC -1- SUBUNIT: Component of a complex containing dpy-26 and two
 CC unidentified proteins.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Associates with chromatin after 30-
 CC cell stage. It specifically localizes to the X chromosomes of
 CC wild-type XX embryos, but remains diffusely distributed throughout
 CC the nuclei of male (XO) embryos. Dpy-26 is required for its X-
 CC chromosome specific association.
 CC -1- DEVELOPMENTAL STAGE: Expressed in embryos and early-staged larvae.
 CC -1- DOMAIN: Consists of two putative central coiled-coil regions
 CC flanked by putative globular regions at the N- and C-termini.
 CC -1- SIMILARITY: Belongs to the SMC family. SMC4 subfamily.
 CC -----
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 CC -----
 DR EMBL: U35274; AA62647.1; -
 DR EMBL: Z35602; CAA84669.1; -
 DR PIR: T24216; T24216.
 DR WormPep: R13G10.1; CE01052.
 DR InterPro: IPR003405; SMC_C.
 DR InterPro: IPR003395; SMC_N.
 DR Pfam: PF02483; SMC_C; 1.
 DR Pfam: PF02463; SMC_N; 1.
 KW DNA condensation; SMC_N; 1.
 DR NP_BIND 122 129
 FT FT NP_BIND 122 129
 FT FT DOMAIN 356 542
 FT FT DOMAIN 543 804
 FT FT DOMAIN 805 974
 FT FT DOMAIN 1016 1056
 FT FT DOMAIN 1159 1182
 FT FT DOMAIN 1245 1280
 FT FT MUTAGEN K->E, I: LOSS OF FUNCTION.
 SQ SEQUENCE 1469 AA; 169618 MW; EF9043CA2AC23B06 CRC64;
 Query Match 67.2%; Score 41; DB 1; Length 1469;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 DDRPYAD 9
 Db 13 DDRPYAD 19
 RESULT 9
 ID AM2A_ORYSA STANDARD; PRT; 443 AA.
 AC P27935;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase isozyme 2A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMY1.5 OR AMY2A.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Japonica M202;
 RC MEDLINE=92175526; PubMed=1541400;
 RA Huang N., Reini S.J., Rodriguez R.L.;
 RT "AMY2A; a novel alpha-amylase-encoding gene in rice.";
 RL Gene 111:223-228(1992).
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING


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CC GERMINATION.
CC CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: M74177; AAA3894.1; -.
DR PIR: J01527; J01527.
DR HSSP: P04063; 1AFA.
DR Gramene: P27941; -.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR KEGG: Glycosidase; Carbohydrate metabolism; Calcium; Signal;
DR MultiGene family.
DR SIGNAL 1 21
DR CHAIN 22 443
DR ACT_SITE 202 202 BY SIMILARITY.
DR ACT_SITE 314 314 BY SIMILARITY.
DR METAL 113 113 CALCIUM (BY SIMILARITY).
DR METAL 172 172 CALCIUM (BY SIMILARITY).
DR SEQUENCE 443 AA; 48527 MW; 783F9264404F67F6 CRC64;

Query Match 65.6%; Score 40; DB 1; Length 443;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDPRYADG 10
Db 146 CRDDTQPSDG 155

RESULT 10
AMC2_ORYSA STANDARD; PRT; 445 AA.
ID AMC2_ORYSA
AC P27941;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase Isozyme C2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.8.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophytidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Indica-IR26; Tissue=Seed;
RA Goldman S., Mawal Y., Wu R.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.

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CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X64619; CA45903.1; -.
DR PIR: S19990; S19990.
DR HSSP: P04063; 1AFA.
DR Gramene: P27941; -.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR KEGG: Glycosidase; Carbohydrate metabolism; Calcium; Signal;
DR MultiGene family.
DR SIGNAL 1 21
DR CHAIN 22 445
DR ACT_SITE 202 202 BY SIMILARITY.
DR ACT_SITE 314 314 BY SIMILARITY.
DR METAL 113 113 CALCIUM (BY SIMILARITY).
DR METAL 172 172 CALCIUM (BY SIMILARITY).
DR SEQUENCE 445 AA; 49207 MW; DED23701E836ACDA CRC64;

Query Match 65.6%; Score 40; DB 1; Length 445;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDDPRYADG 10
Db 146 CRDDTQPSDG 155

RESULT 11
RS6_RHIME STANDARD; PRT; 149 AA.
ID RS6_RHIME
AC O92027;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S6.
DE RPSF OR R01138 OR SMC00568.
GN Rhizobium meliloti (Sinorhizobium meliloti).
OS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RC MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Botte G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Käss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Gallbert F.;
RT Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.
RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
RL -1- FUNCTION: Binds together with S18 to 16S ribosomal RNA (by
RL similarity).
CC -1- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----

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DR EMBL: AL591786; CAC45717.1; -.
 DR HAMAP: MF_00360; -; 1.
 DR InterPro: IPR000529; Ribosomal_S6.
 DR Pfam: PF01250; Ribosomal_S6; 1.
 DR Prodom: PD003809; Ribosomal_S6; 1.
 DR TRIGRAMS: TIGR00166; S6; 1.
 DR PROSITE: PS01048; RIBOSOMAL_S6; FALSE_NEG.
 DR Ribosomal protein; rRNA-binding; Complete proteome.
 KW RIBOSOMAL PROTEIN; rRNA-BINDING; COMPLETE PROTEOME.
 SQ SEQUENCE 149 AA; 17274 MW; 15766B6EAEFF18C CRC64;

Query Match 62.3%; Score 38; DB 1; Length 149;
 Best Local Similarity 77.8%; Pred. No. 4.9;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPYADG 10
 Db 109 RDDRPYADG 117

RESULT 12
 RS6_AGR5 STANDARD; PRT; 153 AA.
 AC 08UG67;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S6.
 GN RPS6 OR ATU1091 OR AGR.C.2022.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 CX NCBI_TaxID=16299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutaydin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quicilis B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Homiel K., Gordon J., Vaundin D., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 CC -1- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
 similarity).
 CC -1- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AE009072; AAL2104.1; -.

DR EMBL: AE008039; -; NOT_ANNOTATED_CDS.
 DR PIR: AB2711; AB2711.
 DR HAMAP: MF_00360; -; 1.
 DR InterPro: IPR000529; Ribosomal_S6.
 DR Pfam: PF01250; Ribosomal_S6; 1.
 DR Prodom: PD003809; Ribosomal_S6; 1.
 DR TRIGRAMS: TIGR00166; S6; 1.
 DR PROSITE: PS01048; RIBOSOMAL_S6; FALSE_NEG.
 DR Ribosomal protein; rRNA-binding; Complete proteome.
 KW RIBOSOMAL PROTEIN; rRNA-BINDING; COMPLETE PROTEOME.
 SQ SEQUENCE 153 AA; 17766 MW; 79C494057455977F CRC64;

Query Match 62.3%; Score 38; DB 1; Length 153;
 Best Local Similarity 77.8%; Pred. No. 5;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RDDRPYADG 10
 Db 109 RDDRPYADG 117

RESULT 13
 VU3_HSV60 STANDARD; PRT; 373 AA.
 AC 001350;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE U3 protein.
 GN U3 OR SHL2.
 OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Betaherpesvirinae; Roseolovirus.
 CX NCBI_TaxID=10370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92333249; PubMed=1321206;
 RA Estathou S., Lawrence G.L., Brown C.M., Barrell B.G.;
 RT "Identification of homologues to the human cytomegalovirus US22 gene
 family in human herpesvirus 6.";
 RL J. Gen. Virol. 73:1661-1671(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95266321; PubMed=7747482;
 RA Campels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
 RA Martin M.E., Efsthathou S., Craxton M., Macaulay H.A.;
 RT "The DNA sequence of human herpesvirus-6: structure, coding content,
 and genome evolution.";
 RL Virology 209:29-51(1995).
 CC -1- SIMILARITY: BELONGS TO THE US22 FAMILY. STRONGEST SIMILARITY TO
 HUMAN CYTOMEGALOVIRUS US24 PROTEIN.
 CC -----
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 CC -----
 DR EMBL: X83413; CAAS8430.1; -.
 DR EMBL: D10082; BAA00977.1; -.
 DR PIR: J01648; J01648.
 DR InterPro: IPR003360; US22.
 DR Pfam: PF02393; US22; 1.
 DR PROSITE: PS01048; RIBOSOMAL_S6; FALSE_NEG.
 DR Ribosomal protein; rRNA-binding; Complete proteome.
 KW RIBOSOMAL PROTEIN; rRNA-BINDING; COMPLETE PROTEOME.
 SQ SEQUENCE 373 AA; 43698 MW; 684A02E7236D274E CRC64;

Query Match 62.3%; Score 38; DB 1; Length 373;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDPYAD 9
 Db 90 CRDDPYAD 98

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.W., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -I- FUNCTION: SEGMENT POLARITY PROTEIN REQUIRED FOR CORRECT PATTERNING
 CC OF EVERY SEGMENT. G PROTEIN-COUPLED RECEPTOR THAT ASSOCIATES WITH
 CC THE PATCHED PROTEIN (PTC) TO TRANSDUCE THE HEDGEHOG (HH) SIGNAL.
 CC THROUGH THE ACTIVATION OF AN INHIBITORY G-PROTEIN. IN THE ABSENCE
 CC OF HH, PTC REPRESENTS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO
 CC THROUGH FUSED (FU).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT ALL DEVELOPMENTAL STAGES, THOUGH
 CC THE LEVELS VARY.
 CC -I- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-9, MET-13 OR MET-14 IS
 CC THE INITIATOR.
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 CC -----
 DR EMBL: U87613; AAC33180.1; -;
 DR EMBL: AF030334; AAB84275.1; -;
 DR EMBL: AE003590; AAF51518.2; -;
 DR Flybase: FBgn0003444; smo.
 DR GO: GO:0007350; P:blastoderm segmentation; IMP.
 DR GO: GO:0007455; P:eye-antennal disc metamorphosis; IGI.
 DR GO: GO:0007346; P:regulation of mitotic cell cycle; IMP.
 DR InterPro: IPR0000539; Fz1zled.
 DR InterPro: IPR000024; Fz_domain.
 DR InterPro: IPR000832; GPCR_secretin.
 DR Pfam: PF01534; Fz1zled; 1.
 DR Pfam: PF01392; Fz; 1.
 DR PRINTS: PRO0489; FRIZLED.
 DR SMART: SM00063; FRI; 1.
 DR PROSITE: PS50038; Fz; 1.
 DR PROSITE: PS50261; G-PROTEIN_RECEP_F2_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW developmental protein.
 FT SIGNAL 1 31
 FT CHAIN 32 1036
 FT DOMAIN 32 258
 FT TRANSMEM 259 279
 FT DOMAIN 280 287
 FT TRANSMEM 288 308
 FT DOMAIN 309 339
 FT TRANSMEM 340 360
 FT DOMAIN 361 381
 FT TRANSMEM 382 402
 FT DOMAIN 403 421
 FT TRANSMEM 422 442
 FT DOMAIN 443 469
 FT TRANSMEM 470 490
 FT DOMAIN 491 532
 FT TRANSMEM 533 553
 FT DOMAIN 554 1036
 FT DOMAIN 85 206
 FT DOMAIN 816 819
 FT CARBOHYD 55 55
 FT CARBOHYD 95 95
 FT CARBOHYD 184 184
 FT CARBOHYD 195 195

FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1036 AA; 116552 MW; 7797FC71A539A87A CRC64;
 Query Match 62.3%; Score 38; DB 1; Length 1036;
 Best Local Similarity 66.7%; Pred No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 RDRPRPADG 10
 Db 68 RDKRPWPDG 76
 ID POLG_LMVE STANDARD; PRT; 3255 AA.
 AC P89676;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [contains: N-terminal protein (P1); Helper
 DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
 DE protein 1 (6k1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 DE (6k2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
 DE (NI-A) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 DE inclusion protein B (NI-B) (NI-B) (RNA-directed RNA polymerase)
 DE (EC 2.7.7.48); Coat protein (CP)].
 OS Lettuce mosaic virus (strain E) (LMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=117132;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97239892; PubMed=9085548;
 RA Revers F., Yang S.-J., Walter J., Souche S., Lot H., Le Gall O.,
 RA Candresse T., Dunez J.;
 RT "Comparison of the complete nucleotide sequences of two isolates of
 RT lettuce mosaic virus differing in their biological properties.";
 RL Virus Res. 47:167-177(1997).
 CC -I- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
 CC -I- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -I- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
 CC further restricted by preferences for the amino acids in P6 - P1'
 CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
 CC Glu(Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(n).
 CC -I- CATALYTIC ACTIVITY: Hydrolyzes a Gly-I-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-I-Gly, in the
 CC processing of the polioviral polypeptide.
 CC -I- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -I- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -I- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -I- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -I- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
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CC EMBL: X97705: CAAG6681.1: -
DR MEMOS: C04.001: -
DR MEMOS: C06.001: -
DR InterPro: IPR001410: DEAD.
DR InterPro: IPR001350: Helicase_C.
DR InterPro: IPR001330: Peptidase_C4.
DR InterPro: IPR001456: Peptidase_C6.
DR InterPro: IPR001592: Poly-coat.
DR InterPro: IPR002540: Poly-PL.
DR InterPro: IPR007095: RNA_pol_DS_PS.
DR InterPro: IPR001205: RNA_pol_PSD.
DR InterPro: IPR007094: RNA_pol_PSVir.
DR Pfam: PF00270: DEAD_1.
DR Pfam: PF00271: Helicase_C_1.
DR Pfam: PF00863: Peptidase_C4_1.
DR Pfam: PF00851: Peptidase_C6_1.
DR Pfam: PF00767: Poly-coat_1.
DR Pfam: PF01577: Poly-PL_1.
DR Pfam: PF00680: RNA_dep_RNA_pol_1.
DR PRINTS: PR00966: NIAPOTYPASE.
DR SMART: SM00487: DEXDC_1.
DR SMART: SM00490: HELIC_1.
KW Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 N-TERMINAL PROTEIN.
FT CHAIN 2 HELPER COMPONENT PROTEINASE.
FT CHAIN 3 PROTEIN P3.
FT CHAIN 4 6 KDa PROTEIN 1.
FT CHAIN 5 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 6 6 KDa PROTEIN 2.
FT CHAIN 7 GNOSE-LINKED PROTEIN.
FT CHAIN 8 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 9 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 10 COAT PROTEIN.
FT NP_BIND 2978 3255
FT NP_BIND 1410 1417
SQ SEQUENCE 3255 AA; 367618 MW; B358582927E01628 CRC64;

Query Match 62.3%; Score 38; DB 1; Length 3255;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDRPYAD 9
DB 2915 CLDEAPYAD 2923

RESULT 17
NGF_CHICK STANDARD; PRT; 243 AA.
AC POS200:
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF).
GN NGFB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBT_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86300646; PubMed=3017695;
RT Ebendahl T., Larhammar D., Persson H.;
RT "Structure and expression of the chicken beta nerve growth factor
RT gene.";
RL EMBO J. 5:1483-1487(1986).
RN [2]
RP SEQUENCE OF 118-243 FROM N.A.
RX MEDLINE=86248129; PubMed=3720959;
RT Wion D., Perret C., Frechin N., Keller A., Behar G., Brachet P.,

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RA Aulfray C.;
RT Molecular cloning of the avian beta-nerve growth factor gene:
RT transcription in brain.";
RL FEBS Lett. 203:82-86(1986).
RN [3]
RP SEQUENCE OF 121-243 FROM N.A.
RX MEDLINE=86300647; PubMed=2427334;
RA Weiler R., Becker-Andre M., Goltz R., Heumann R., Shaw A., Thoenen H.;
RT "Molecular cloning of bovine and chick nerve growth factor (NGF):
RT delineation of conserved and unconserved domains and their
RT relationship to the biological activity and antigenicity of NGF.";
RL EMBO J. 5:1489-1493(1986).
RN [4]
RP SEQUENCE OF 181-222 FROM N.A.
RX MEDLINE=91222573; PubMed=2025430;
RA Halboeck F., Ibanez C.F., Persson H.;
RT "Evolutionary studies of the nerve growth factor family reveal a
RT novel member abundantly expressed in Xenopus ovary.";
RL Neuron 6:845-858(1991).
CC -1- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC SYMPATHETIC SENSORY NEURONS.
CC -1- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -1- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X04003; CA27633.1; ALT_INT.
DR EMBL: X04067; CA27703.1; -
DR EMBL: M26810; AAA48984.1; -
DR PIR: A26311; A26311.
DR HSSP: P01139; 1BET.
DR InterPro: IPR002072; NGF.
DR Pfam: PF00243; NGF_1.
DR PRINTS: PR00268; NGF.
DR PRODOM: PD002052; NGF_1.
DR SMART: SM00140; NGF_1.
DR PROSITE: PS00248; NGF_1; 1.
DR PROSITE: PS0270; NGF_2; 1.
KW Growth factor; Signal.
FT SIGNAL 1 22
FT PROPEP 23 125
FT CHAIN 126 243 BETA-NERVE GROWTH FACTOR.
FT DISULFID 135 204 BY SIMILARITY.
FT DISULFID 182 232 BY SIMILARITY.
FT DISULFID 192 234 BY SIMILARITY.
SQ SEQUENCE 243 AA; 27138 MW; 74C306CB2079DA07 CRC64;

Query Match 60.7%; Score 37; DB 1; Length 243;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRDDRPYADG 10
DB 182 CRDPRVSSG 191

RESULT 18
PCRB_SACER STANDARD; PRT; 546 AA.
ID PCRB_SACER
AC P53003:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Propionyl-CoA carboxylase beta chain (EC 6.4.1.3) (pCCase) (Propionyl-
DE CoA:carbon dioxide ligase).

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GN  PCOB.
OS  Saccharopolyspora erythraea (Streptomyces erythraeus).
OC  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC  Pseudonocardineae; Pseudonocardiaceae; Saccharopolyspora.
OX  NCBI_TaxID=1836;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=NRRL 2336;
RA  MEDLINE=96249691; PubMed=8830278;
RX  Donadio S., Staver M.J., Katz L.;
RT  "Erythromycin production in Saccharopolyspora erythraea does not
RL  require a functional propionyl-CoA carboxylase."
RM  Mol. Microbiol. 19:977-984(1996).
CC  -1- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3)(-) = ADP +
CC  phosphate + (S)-methylmalonyl-CoA.
CC  -1- PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF ODD-CHAIN
CC  FATTY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.
CC  -1- SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX BIOTIN-CONTAINING
CC  ALPHA SUBUNITS & SIX BETA SUBUNITS (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE ACCD / PCOB FAMILY.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: X92557; CAA63310.1; -.
DR  PIR: S71008.
DR  InterPro: IPR000438; ACOACC_transf.
DR  InterPro: IPR000022; Carboxyl_trans.
DR  Pfam: PF01039; Carboxyl_trans. 1.
DR  PRINTS: PR01070; ACCCTFRASEB.
DR  LIGASE.
KM  SEQUENCE 546 AA; 58526 MW; 96A38CA77FC68C5 CRC64;
SQ
Query Match 60.7%; Score 37; DB 1; Length 546;
Best Local Similarity 85.7%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 4 DRPYADG 10
    |||||
Db 87 DRPYGDG 93

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RL  Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: Likely to be an important mediator of ventricular
CC  differentiation during cardiac development.
CC  -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC  -1- TISSUE SPECIFICITY: Predominantly expressed in cardiac ventricles.
CC  -1- SIMILARITY: BELONGS TO THE TALE/IRO HOMEOBOX FAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AF124733; AAF23887.1; -.
DR  EMBL: U90306; AAB50004.1; -.
DR  HSSP: PA1778; IDU6.
DR  TRANSFAC: T04275; -.
DR  Genew: HGNC:6129; IRX4.
DR  MIM: 606199; -.
DR  GO: GO:0007507; P:heart development; TAS.
DR  InterPro: IPR001356; Homeobox.
DR  InterPro: IPR003893; Iroquois_homeo.
DR  Pfam: PF00046; homeobox. 1.
DR  ProDom: PD000010; Homeobox; 1.
DR  SMART: SM00389; HOX; 1.
DR  SMART: SM00548; IRO; 1.
DR  PROSITE: PS00027; HOMEOBOX_1; 1.
DR  PROSITE: PS50071; HOMEOBOX_2; 1.
KM  Homeobox: DNA-binding; Nuclear protein.
FT  DNA_BIND 143 204 HOMEOBOX (TALE-TYPE).
FT  DOMAIN 223 228 POLY-GLU.
FT  DOMAIN 375 382 POLY-ALA.
FT  CONFLICT 181 181 I -> T (IN REF. 2).
SQ
Query Match 59.8%; Score 36.5; DB 1; Length 519;
Best Local Similarity 63.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
Oy 1 CRDD-RPYADG 10
    |||:|||||
Db 214 CADKRRPYAEG 224

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RESULT 19
IRX4_HUMAN
ID IRX4_HUMAN STANDARD: PRT: 519 AA.
AC P78413; O90HR2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Iroquois-class homeodomain protein IRX-4 (Iroquois homeobox protein
DE 4).
GN IRX4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20092750; PubMed=10625552;
RX Bruneau B.G., Bao Z.-Z., Tanaka M., Schott J.J., Izumo S., Cepko C.L.,
RA Seidman J.G., Seidman C.E.;
RT "Cardiac expression of the ventricle-specific homeobox gene Irx4 is
RT modulated by Nkx2-5 and dHAND."
RL Dev. Biol. 217:266-277(2000).
RN [2]
RP SEQUENCE OF 80-191 FROM N.A.
RA Lewis M.T., Strickland P.A., Ross S., Snyder C.J., Daniel C.W.;
RT "IRX: a new family of human homeobox genes from the breast."

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RESULT 20
TRMD_BUCAL
ID TRMD_BUCAL STANDARD: PRT: 237 AA.
AC P57476;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-methyltransferase (EC 2.1.1.31) (MG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR BU396.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -----
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF001119; BABI3099.1; -.
DR HAMAP: MF_00605; -.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
SQ SEQUENCE 237 AA; 27335 MW; 86CE3836B3EC4AB CRC64;

Query Match          59.0%; Score 36; DB 1; Length 237;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
   |||||
DB 59 DDRPYGCG 66

RESULT 21
TRMD_PASMT
ID TRMD_PASMT STANDARD; PRT; 245 AA.
DC 00CLE1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
TM MD OR PM1297.
GN Pasteurella multocida.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RA MEDLINE-21145866; PubMed-11248100;
RA May B.J., Zhang Q., Li L., Paustian M.L., Whittam T.S., Kapur V.;
RA "Complete genome sequence of Pasteurella multocida Pm70.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: AE006168; AAR0381.1; -.
DR HAMAP: MF_00605; -.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNA (Guanine-N(1)-)-methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 245 AA; 27494 MW; 6A35655295A59354 CRC64;
```

```
Query Match          59.0%; Score 36; DB 1; Length 245;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DDRPYADG 10
   |||||
DB 50 DDRPYGCG 57

RESULT 22
TRMD_HAEIN
ID TRMD_HAEIN STANDARD; PRT; 246 AA.
AC P43912;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
TM MD OR H10202.
GN Haemophilus influenzae.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RA MEDLINE-95350630; PubMed-7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uiterback T.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: U32705; AAC21871.1; -.
DR PIR: G64054; G64054.
DR TIGR: H10202; G64054.
DR HAMAP: MF_00605; -.
DR InterPro: IPR002649; tRNA_mIG_MT.
DR Pfam: PF01746; tRNA_mIG_MT.1.
DR ProDom: PD004978; tRNA_mIG_MT.1.
DR TIGRFAMs: TIGR00088; tmd; 1.
KW tRNA (Guanine-N(1)-)-methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 246 AA; 27542 MW; DEEF238159B1003D CRC64;
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RESULT 23
TRMD_YERPE STANDARD; PRT; 246 AA.
ID TRMD_YERPE
AC O82B09: O8CWH8;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR YPO3293 OR Y0896.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahitha M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Medisevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Heffernon J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC
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CC -----
DR EMBL: AJ414156; CAC92525.1; -
DR EMBL: AE013692; AAM84480.1; ALT_INIT.
DR PIR: A10399; A10399.
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT; 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRFAMs: TIGR00088; trmd; 1.
DR TRANSFERASE: Methyltransferase; tRNA processing; Complete proteome.
KW SEQUENCE 246 AA; 27618 MW; DB800072F976ABCE CRC64;
SQ
Query Match 59.0%; Score 36; DB 1; Length 246;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 DDRPYADG 10
| | | | |
DB 50 DDRPYGGG 57

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RESULT 24
TRMD_VIBVU STANDARD; PRT; 249 AA.
ID TRMD_VIBVU
AC O8CWH5;
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR V11617.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RX Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC
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CC -----
DR EMBL: AE016802; AAO10036.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT; 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRFAMs: TIGR00088; trmd; 1.
KW TRANSFERASE: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 249 AA; 28157 MW; B1CF66BC5D3451 CRC64;
SQ
Query Match 59.0%; Score 36; DB 1; Length 249;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 DDRPYADG 10
| | | | |
DB 50 DDRPYGGG 57

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CC SPECIES-E.colli: STRAIN-K12: RX MEDLINE-97349980: Pubmed-9205837: RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., RA Itoh T., Kimura S., Kitagawa M., Makino T., Miki T., Mitsunashi N., RA Mizuchuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H., RA Oshima T., Oyama S., Saito N., Sempel G., Setoh Y., Sivasubram S., RA Tagami H., Takahashi H., Tanaka J., Yamamoto K., Yehara K., Wada C., RA Yamagata S., Horiiuchi F., RT Construction of a contiguous 874-kb sequence of the *Escherichia coli* RT K12 genome corresponding to 50.0-68.6 min on the linkage map and RT analysis of its sequence features. Proc. Natl. Acad. Sci. U.S.A. 99:11020-17024(2002).

CC SPECIES-E.colli: STRAIN-06.H1 / CFT073 / ATCC 700928: RX MEDLINE-22388234: Pubmed-12471157: RA Welch R.A., Burland V., Plunkett G., III, Redford P., Roesch P., RA Rasko D., Buckles E.L., Liao S.-R., Boulin A., Hackett J., Stroud D., RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., RA Mobley H.L.T., Donenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*." Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

CC SPECIES-E.colli: STRAIN-0157.H7 / EDL933 / ATCC 700927: RX MEDLINE-21074935: Pubmed-11206551: RA Perna N.T., Plunkett G., IV, Burland V., Mau B., Glasner J.D., RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., RA Grobicki E.J., Davis N.W., Llin A., Dialaite E.T., Potomous K., RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., RA Welch R.A., Blattner F.R.; "Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7." Nature 409:529-533(2001).

CC SPECIES-E.colli: STRAIN-0157.H7 / RMD 0509952: RX MEDLINE-21156231: Pubmed-11258796: RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K., RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., RA Iida T., Takama H., Honda T., Sasaoka C., Ogasawara N., Yasunaga T., RA Kihara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12." DNA Res. 8:11-22(2001).

CC SPECIES-S.flexneri: STRAIN-101 / serotype 2a: RX MEDLINE-2272406: Pubmed-12845590: RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., RA Yan J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., RA Sun L., Xue Y., Zhao A., Gao Y., Zhu D., Qian B., Ding K., Chen S., RA Cheng H., Yao Z., He B., Chen R., Ma J., Kang B., Wen Y., Hou Y., Yu J.; "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157." Nucleic Acids Res. 30:4432-4441(2002).

CC CHARACTERIZATION, AND SEQUENCE OF 1-10. RX SPECIES-E.colli: MEDLINE-83108856: Pubmed-6337336: RA Hjalmarsson K.-J., Byström A.S., Björk G.R.; "Purification and characterization of transfer RNA (guanine-1-methyltransferase from *Escherichia coli*." J. Biol. Chem. 268:1343-1351(1993).

CC FUNCTION: Specifically methylates guanosine-37 in various tRNAs. CC CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing N(1)-methylguanine.

CC SUBUNIT: Monomer.

CC SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC MISCELLANEOUS: THE SPECIFIC ACTIVITY OF THIS ENZYME INCREASES ONLY SLIGHTLY WITH INCREASED GROWTH RATE.

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CC -1- MISCELLANEOUS: THIS ENZYME IS PRESENT AT CA. 80 MOLECULES/GENOME.
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: X01818; CA25959.1; -
DR EMBL: AE000346; AAC75656.1; -
DR EMBL: D90888; BA16492.1; -
DR EMBL: AE016764; AA81578.1; -
DR EMBL: AE005490; AA657718.1; -
DR EMBL: AP002562; BAB36893.1; -
DR EMBL: AE015282; AAN44162.1; -
DR PIR: A30380; XHECC1.
DR PIR: B85907; B85907.
DR PIR: F91062; F91062.
DR EcoGene: EG11023; trmd.
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT. 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRfams: TIGR00088; trmd; 1.
DR TransfErse: Methyltransferase; tRNA processing. Complete proteome.
SQ SEQUENCE 255 AA; 28422 MW; B101087229B4CDBD CRC64;

Query Match 59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
Db 50 DDRPYGGG 57

RESULT 27
TRMD_SALTY
ID TRMD_SALTY STANDARD; PRT; 255 AA.
AC 082415;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR STY2861 OR T2629.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; Pubmed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jorgels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Goora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RA enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; Pubmed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

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RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RA and CT18."
RL 185:2330-2337(2003).
RC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (by similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL627276; CAD05853.1; -
DR EMBL: AE016843; AA070200.1; -
DR HAMAP: MF_00605; -; 1.
DR InterPro: IPR002649; tRNA_m1G_MT.
DR Pfam: PF01746; tRNA_m1G_MT; 1.
DR ProDom: PD004978; tRNA_m1G_MT; 1.
DR TIGRfams: TIGR00088; trmd; 1.
DR TransfErse: Methyltransferase; tRNA processing. Complete proteome.
SQ SEQUENCE 255 AA; 28318 MW; B96812A32091495F CRC64;

Query Match 59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDRPYADG 10
Db 50 DDRPYGGG 57

RESULT 28
TRMD_SALTY
ID TRMD_SALTY STANDARD; PRT; 255 AA.
AC P36245;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1)-)-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR STW2674.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Persson B.C.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SCSA1412 / ATCC 700720;
RX MEDLINE=21534948; Pubmed=11677609;
RA McClelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RA LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; Pubmed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA "Complete genome sequence of a multiple drug resistant Salmonella
RA enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; Pubmed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC -----
DR EMBL: X74933; CAAS2887.1; -.
DR EMBL: AE008821; AL21563.1; -.
DR PIR: S37175; S37175.
DR StryGene: SG10395; trmd.
DR HAMAP: MF_00605; -. 1.
DR InterPro: IPR002649; tRNA_mlg_MT.
DR Pfam: PF01746; tRNA_mlg_MT; 1.
DR ProDom: PD004978; tRNA_mlg_MT; 1.
DR TIGRfams: TIGR00088; trmd; 1.
DR KW Transferase: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 255 AA; 28348 MW; A5691ED3CE1495F CRC64;

Query Match          59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 50 DDPRYGGG 57

RESULT 29
TRMD_SERMA
ID TRMD_SERMA STANDARD; PRT; 255 AA.
AC P36244;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1))-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAYN-SM6;
RX MEDLINE-9432077; PubMed-8045416;
RA Jin S., Benedix M.O.;
RT "Sequences of the Serratia marcescens rplS and trmd genes.";
RL Gene 145:147-148(1994).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L23334; AAM50783.1; -.
DR HAMAP: MF_00605; 1.
DR InterPro: IPR002649; tRNA_mlg_MT.
DR Pfam: PF01746; tRNA_mlg_MT; 1.
DR ProDom: PD004978; tRNA_mlg_MT; 1.
DR TIGRfams: TIGR00088; trmd; 1.
DR KW Transferase: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 262 AA; 30500 MW; 653A65B1663A04CA CRC64;

Query Match          59.0%; Score 36; DB 1; Length 262;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 67 DDPRYGGG 74

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DR TIGRfams: TIGR00088; trmd; 1.
DR KW Transferase: Methyltransferase; tRNA processing.
SQ SEQUENCE 255 AA; 28465 MW; 48A71576D9B3A50B CRC64;

Query Match          59.0%; Score 36; DB 1; Length 255;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 50 DDPRYGGG 57

RESULT 30
TRMD_BUCAP
ID TRMD_BUCAP STANDARD; PRT; 262 AA.
AC O8K9F4;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE tRNA (Guanine-N(1))-methyltransferase (EC 2.1.1.31) (MIG-
DE methyltransferase) (tRNA [GM37] methyltransferase).
GN TRMD OR B0SG383;
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-22084549; PubMed-12089438;
RA Tames I., Klason L., Canbeek B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Anderson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -1- FUNCTION: Specifically methylates guanosine-37 in various tRNAs
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(1)-methylguanine.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE014114; AAM67935.1; -.
DR InterPro: IPR002649; tRNA_mlg_MT.
DR Pfam: PF01746; tRNA_mlg_MT; 1.
DR ProDom: PD004978; tRNA_mlg_MT; 1.
DR TIGRfams: TIGR00088; trmd; 1.
DR KW Transferase: Methyltransferase; tRNA processing; Complete proteome.
SQ SEQUENCE 262 AA; 30500 MW; 653A65B1663A04CA CRC64;

Query Match          59.0%; Score 36; DB 1; Length 262;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DDPRYADG 10
Db 67 DDPRYGGG 74

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Search completed: August 29, 2003, 18:45:12
 Job time : 8.57145 secs

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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:40:26 ; Search time 24.5714 Seconds
(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-2
Perfect score: 61
Sequence: 1 CRDPRPADG 10

Scoring table: BLOSUM62
Gap0 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP virus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 61 | 100.0 | 427 | 10 | Q40015 hordeum vul |
| 2 | 61 | 100.0 | 427 | 10 | Q03651 hordeum vul |
| 3 | 56 | 91.8 | 429 | 10 | Q40016 hordeum vul |
| 4 | 47 | 77.0 | 421 | 10 | Q42504 hordeum vul |
| 5 | 47 | 77.0 | 437 | 10 | Q04965 hordeum vul |
| 6 | 44 | 72.1 | 416 | 10 | Q08106 hordeum vul |
| 7 | 44 | 72.1 | 416 | 10 | Q08GUR0 hordeum vul |
| 8 | 44 | 72.1 | 437 | 10 | Q04964 hordeum vul |
| 9 | 44 | 72.1 | 437 | 10 | Q40018 hordeum vul |
| 10 | 44 | 72.1 | 438 | 10 | Q40017 hordeum vul |
| 11 | 42 | 68.9 | 434 | 10 | Q081699 hordeum vul |
| 12 | 42 | 68.9 | 437 | 10 | Q081700 avena fatua |
| 13 | 41 | 67.2 | 278 | 10 | Q04272 oryza sativ |
| 14 | 41 | 67.2 | 420 | 10 | Q02P43 phaseolus v |
| 15 | 41 | 67.2 | 423 | 10 | Q42678 cuscuta ref |
| 16 | 41 | 67.2 | 424 | 10 | Q81P27 pharbitis n |

| | | | | | |
|----|------|------|------|----|--------|
| 17 | 41 | 67.2 | 1593 | 5 | Q85X82 |
| 18 | 41 | 67.2 | 2871 | 5 | Q9V483 |
| 19 | 41 | 67.2 | 2871 | 5 | Q81M87 |
| 20 | 40 | 65.6 | 248 | 16 | Q8Z874 |
| 21 | 40 | 65.6 | 266 | 16 | Q8D041 |
| 22 | 40 | 65.6 | 105 | 16 | Q92R82 |
| 23 | 39.5 | 64.8 | 175 | 16 | Q93J13 |
| 24 | 39 | 63.9 | 144 | 16 | Q50398 |
| 25 | 39 | 63.9 | 370 | 16 | Q9A976 |
| 26 | 39 | 63.9 | 382 | 16 | Q98778 |
| 27 | 39 | 63.9 | 556 | 5 | Q9NG23 |
| 28 | 39 | 63.9 | 594 | 5 | Q9Y113 |
| 29 | 39 | 63.9 | 642 | 5 | Q8MPM6 |
| 30 | 39 | 63.9 | 739 | 5 | Q9G524 |
| 31 | 39 | 63.9 | 742 | 5 | Q818V3 |
| 32 | 39 | 63.9 | 872 | 16 | Q8PJW3 |
| 33 | 39 | 63.9 | 1285 | 16 | Q8DA47 |
| 34 | 38 | 62.3 | 109 | 10 | Q94D61 |
| 35 | 38 | 62.3 | 386 | 12 | Q9WT61 |
| 36 | 38 | 62.3 | 449 | 10 | Q9AV79 |
| 37 | 38 | 62.3 | 449 | 10 | Q9AV79 |
| 38 | 38 | 62.3 | 795 | 10 | Q9AYF1 |
| 39 | 38 | 62.3 | 740 | 2 | Q93GV9 |
| 40 | 37 | 60.7 | 42 | 6 | Q02794 |
| 41 | 37 | 60.7 | 136 | 5 | Q9NHL9 |
| 42 | 37 | 60.7 | 253 | 2 | Q03093 |
| 43 | 37 | 60.7 | 254 | 5 | Q9U718 |
| 44 | 37 | 60.7 | 325 | 10 | Q93700 |
| 45 | 37 | 60.7 | 413 | 4 | Q96R64 |
| 46 | 37 | 60.7 | 413 | 4 | Q99984 |
| 47 | 37 | 60.7 | 463 | 5 | Q9N2M4 |
| 48 | 37 | 60.7 | 463 | 5 | Q22347 |
| 49 | 37 | 60.7 | 510 | 2 | Q8K441 |
| 50 | 37 | 60.7 | 521 | 16 | Q9A9P5 |
| 51 | 37 | 60.7 | 766 | 4 | P82987 |
| 52 | 37 | 60.7 | 857 | 13 | P79708 |
| 53 | 37 | 60.7 | 1023 | 4 | Q9UL17 |
| 54 | 37 | 60.7 | 1083 | 2 | Q8KRR8 |
| 55 | 37 | 60.7 | 1417 | 10 | Q9AX82 |
| 56 | 37 | 60.7 | 1450 | 10 | Q8GUR8 |
| 57 | 37 | 60.7 | 6521 | 2 | Q8RL72 |
| 58 | 37 | 60.7 | 6521 | 2 | Q8RL72 |
| 59 | 36 | 59.0 | 133 | 9 | Q9T166 |
| 60 | 36 | 59.0 | 173 | 16 | Q98CT9 |
| 61 | 36 | 59.0 | 194 | 5 | Q8SVU7 |
| 62 | 36 | 59.0 | 248 | 16 | Q8CX44 |
| 63 | 36 | 59.0 | 249 | 16 | Q8CWM5 |
| 64 | 36 | 59.0 | 258 | 2 | Q52599 |
| 65 | 36 | 59.0 | 265 | 16 | Q8CWM8 |
| 66 | 36 | 59.0 | 282 | 16 | Q9S208 |
| 67 | 36 | 59.0 | 349 | 10 | Q41441 |
| 68 | 36 | 59.0 | 418 | 5 | Q9CTK1 |
| 69 | 36 | 59.0 | 446 | 17 | Q9HHJ9 |
| 70 | 36 | 59.0 | 482 | 16 | Q8KYN7 |
| 71 | 36 | 59.0 | 516 | 16 | Q9CD09 |
| 72 | 36 | 59.0 | 537 | 16 | Q9ZLC7 |
| 73 | 36 | 59.0 | 1123 | 5 | Q18431 |
| 74 | 36 | 59.0 | 1181 | 16 | Q8G6E4 |
| 75 | 36 | 59.0 | 4834 | 4 | Q95714 |
| 76 | 35.5 | 58.2 | 286 | 10 | Q9ZTE1 |
| 77 | 35.5 | 58.2 | 280 | 10 | Q9LXV2 |
| 78 | 35.5 | 58.2 | 280 | 10 | Q9LXV2 |
| 79 | 35 | 57.4 | 118 | 16 | Q9WYE4 |
| 80 | 35 | 57.4 | 118 | 16 | Q942R7 |
| 81 | 35 | 57.4 | 153 | 5 | Q16208 |
| 82 | 35 | 57.4 | 196 | 10 | Q9SJA6 |
| 83 | 35 | 57.4 | 207 | 16 | Q8XW6 |
| 84 | 35 | 57.4 | 225 | 12 | Q8B0X3 |
| 85 | 35 | 57.4 | 269 | 10 | Q8B0C9 |
| 86 | 35 | 57.4 | 270 | 10 | Q81934 |
| 87 | 35 | 57.4 | 295 | 2 | Q54379 |
| 88 | 35 | 57.4 | 330 | 2 | Q8GP47 |
| 89 | 35 | 57.4 | 338 | 10 | Q942E4 |
| 90 | 35 | 57.4 | 340 | 11 | Q8BR07 |

| | |
|--------|-------------|
| Q85X82 | drosophila |
| Q9V483 | drosophila |
| Q81M87 | drosophila |
| Q8Z874 | yeastina pe |
| Q8D041 | yeastina pe |
| Q92R82 | rhizobium m |
| Q93J13 | streptomyce |
| Q50398 | mycobacteri |
| Q9A976 | caulobacter |
| Q98778 | rhizobium I |
| Q9NG23 | giardia lam |
| Q9Y113 | drosophila |
| Q8MPM6 | giardia lam |
| Q9G524 | giardia lam |
| Q818V3 | giardia lam |
| Q8PJW3 | xanthomonas |
| Q8DA47 | vibrio vuln |
| Q94D61 | oryza sativ |
| Q9WT61 | human herpe |
| Q9AV79 | oryza sativ |
| Q9AV79 | oryza sativ |
| Q93GV9 | streptomyce |
| Q9AYF1 | oryza sativ |
| Q02794 | ornithorhyn |
| Q9NHL9 | plasmidium |
| Q03093 | streptomyce |
| Q9U718 | plasmidium |
| P82987 | vigna ungu |
| P79708 | homo sapien |
| Q9UL17 | homo sapien |
| Q8KRR8 | caulobacter |
| Q9AX82 | oryza sativ |
| Q8GUR8 | oryza sativ |
| Q8RL72 | plasmidom |
| Q8RL72 | plasmidom |
| Q9T166 | bacterioph |
| Q98CT9 | rhizobium I |
| Q8SVU7 | encephalito |
| Q8CX44 | shewanella |
| Q8CWM5 | vibrio vuln |
| Q52599 | agrobacteri |
| Q8CWM8 | yeastina pe |
| Q9S208 | streptomyce |
| Q41441 | solanum tub |
| Q9CTK1 | hydra atten |
| Q9HHJ9 | halobacteri |
| Q8KYN7 | clostridium |
| Q9CD09 | mycobacteri |
| Q9ZLC7 | rhizobium m |
| Q18431 | caenorhabd |
| Q8G6E4 | bilidobacte |
| Q95714 | homo sapien |
| Q9ZTE1 | arbidopsis |
| Q9LXV2 | arbidopsis |
| Q9WYE4 | thermotoga |
| Q942R7 | oryza sativ |
| Q16208 | caenorhabd |
| Q9SJA6 | arbidopsis |
| Q8XW6 | raistonia s |
| Q8B0X3 | peanut clum |
| Q8B0C9 | vigna ungu |
| Q81934 | canavalia e |
| Q54379 | streptomyce |
| Q8GP47 | streptococc |
| Q942E4 | oryza sativ |
| Q8BR07 | mus musculi |

| | | | | | |
|-----|----|------|-----|----|--------|
| 90 | 35 | 57.4 | 353 | 16 | Q8PPM1 |
| 91 | 35 | 57.4 | 352 | 16 | Q8P586 |
| 92 | 35 | 57.4 | 360 | 2 | O88000 |
| 93 | 35 | 57.4 | 362 | 2 | O45379 |
| 94 | 35 | 57.4 | 443 | 10 | O9T0A1 |
| 95 | 35 | 57.4 | 469 | 16 | P74685 |
| 96 | 35 | 57.4 | 474 | 5 | O8SV03 |
| 97 | 35 | 57.4 | 485 | 12 | O9DM55 |
| 98 | 35 | 57.4 | 553 | 16 | O9XA97 |
| 99 | 35 | 57.4 | 554 | 16 | O8NMNO |
| 100 | 35 | 57.4 | 576 | 16 | O8XV03 |

ALIGNMENTS

RESULT 1
Q40015 PRELIMINARY; PRT; 427 AA.

AC Q40015; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Barley (H.vulgaris) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Southan B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RT barley.";
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M17125; AAA32925.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro; IPR006047; Alpha-amyl_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 SQ SEQUENCE 427 AA; 47402 MW; D21BA12EAE5F3534 CRC64;

Query Match 100.0%; Score 61; DB 10; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 Db 148 CRDDRYPADG 157

RESULT 2
Q03651

PRELIMINARY; PRT; 427 AA.

AC Q03651; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1).
 GN AMY46.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Himalaya;

RX MEDLINE=89066691; PubMed=3264283;
 RA Khushf B., Rogers J.C.;
 RT "Barley alpha-amylase genes. Quantitative comparison of steady-state
 RT mRNA levels from individual members of the two different families
 RT expressed in aleurone cells.";
 RL J. Biol. Chem. 263:18953-18960(1988).
 DR EMBL; J04202; AAA98615.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro; IPR006047; Alpha-amyl_cat.
 DR InterPro; IPR006589; Alp-amyl_cat_sub.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT CHAIN 26 427
 FT SIGNAL 1 25
 FT POTENTIAL.
 FT ALPHA-AMYLASE.
 SQ SEQUENCE 427 AA; 47456 MW; 5A7496B9E6643824 CRC64;

Query Match 100.0%; Score 61; DB 10; Length 427;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 Db 148 CRDDRYPADG 157

RESULT 3
Q40016

PRELIMINARY; PRT; 429 AA.

AC Q40016; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Barley (H.vulgaris) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Knox C.A.P., Southan B., Chandra G.R., Muthukrishnan S.;
 RT "Structure and organization of two divergent alpha-amylase genes from
 RT barley.";
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M17125; AAA32926.1; -.
 DR HSSP; P04063; IAVA.
 DR InterPro; IPR006047; Alpha-amyl_cat.
 DR InterPro; IPR006589; Alp-amyl_cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 429 AA; 47970 MW; 4E7B8B741C944095 CRC64;

Query Match 91.8%; Score 56; DB 10; Length 429;
 Best Local Similarity 90.0%; Pred. No. 0.041;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRDDRYPADG 10
 Db 148 CRDDRYPADG 157

RESULT 4
Q42504

PRELIMINARY; PRT; 421 AA.

AC Q42504; 01-NOV-1996 (TREMBlrel. 01, Created)

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DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE Alpha-amylase type A.
GN AMY1 OR AMY32B.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Whittier R.F., Dean D.A., Rogers J.C.;
RL Nucleic Acids Res. 13:0-0(1987).
RN [2]
RP SEQUENCE OF 1-46 FROM N.A.
RX MEDLINE=85006965; PubMed=6090459;
RA Rogers J.C., Millman C.;
RT "Coordinate increase in major transcripts from the high pi alpha-
RT amylase multigene family in barley aleurone cells stimulated with
RT gibberellic acid."
RL J. Biol. Chem. 259:12234-12240(1984).
RN [3]
RP SEQUENCE FROM N.A.
RA Whittier R.F., Dean D.A., Rogers J.C.;
RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL: X05186; CAA28803.1; -.
DR EMBL: M15208; AAA32935.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha.amyl_cat.
DR InterPro: IPR006589; Alp.amyl_cat_sub.
DR Pfam: PR00128; alpha-amylase_13.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amyy; 1.
SQ SEQUENCE 421 AA; 46102 MW; 7E43D13A75ACB56 CRC64;

Query Match 77.0%; Score 47; DB 10; Length 421;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
DB 148 CRDPRYADG 157

RESULT 5
AC 004965; PRELIMINARY; PRT; 437 AA.
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN AMY.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews P.R., Gubler F., Jacobsen J.V.;
RT "A plant-based expression system for matching cDNA clones and
RT isoforms." (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: L11277; CAA72144.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha.amyl_cat.
DR InterPro: IPR006589; Alp.amyl_cat_sub.
DR Pfam: PF00128; alpha-amylase_1.
DR SMART: SM00642; Amyy; 1.
DR Glycosylase: Hydrolase.
KW SEQUENCE 437 AA; 47770 MW; 67E910E7CB7769E4 CRC64;
SQ SEQUENCE 437 AA; 47770 MW; 67E910E7CB7769E4 CRC64;

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Query Match 77.0%; Score 47; DB 10; Length 437;
Best Local Similarity 80.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
DB 148 CRDPRYADG 157

RESULT 6
AC 08LJ06; PRELIMINARY; PRT; 416 AA.
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RA Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
RT "Sequencing and molecular characterization of a banana alpha-amylase
RT cDNA clone related to the fruit ripening."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF533648; AAN01149.1; -.
DR InterPro: IPR006047; Alpha.amyl_cat.
DR InterPro: IPR006589; Alp.amyl_cat_sub.
DR Pfam: PF00128; alpha-amylase_13.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amyy; 1.
DR SIGNAL: 1 15 POTENTIAL.
FT CHAIN 16 416 ALPHA-AMYLASE.
FT SIGNAL 1 15 POTENTIAL.
SQ SEQUENCE 416 AA; 46798 MW; 590CFA3A92EEDC45 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 416;
Best Local Similarity 70.0%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
DB 139 CRDPRYADG 148

RESULT 7
AC 08GUR0; PRELIMINARY; PRT; 416 AA.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Nanicao; TISSUE=leaf;
RA Vieira A. Jr., Nascimento J.R.O., Lajolo F.M.;
RT "Sequencing and molecular characterization of a banana alpha-amylase
   RT gene.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY171068; M0011776.1; -.
FW SIGNAL: Hydrolyase; Glycosidase.
KM SIGNAL: 1 15 POTENTIAL.
FT CHAIN 16 416 ALPHA-AMYLASE.
SQ SEQUENCE 416 AA; 4658 MW; 7D5ECE630F221915 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 416;
Best Local Similarity 70.0%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
Db 139 CRDRTKYS DG 148

RESULT 8
O04964 PRELIMINARY; PRT; 437 AA.
AC O04964;
DT 01-JUL-1997 (TREMUREL. 04, Created)
DT 01-JUL-1997 (TREMUREL. 04, Last sequence update)
DT 01-MAR-2003 (TREMUREL. 23, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
GN AMY.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Matthews P.R., Gubler F., Jacobsen J.V.;
RT "A plant-based expression system for matching cDNA clones and
   RT isozymes.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y11276; CAAT2143.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KM Glycosidase; Hydrolyase.
SQ SEQUENCE 437 AA; 4776 MW; E163524C88CB2480 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 437;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
Db 148 CRDRTKYS DG 157

RESULT 9
O04018 PRELIMINARY; PRT; 437 AA.
AC O04018;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-MAR-2003 (TREMUREL. 23, Last annotation update)
DE Barley (H.vulgare) alpha-amylase 2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;

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RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
   RT barley.";
RL Plant Mol. Biol. 9:3-17(1987).
DR EMBL: M17127; AAA32928.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 437 AA; 4781 MW; 68866B0A1A650656 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 437;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
Db 148 CRDRTKYS DG 157

RESULT 10
O04017 PRELIMINARY; PRT; 438 AA.
AC O04017;
DT 01-NOV-1996 (TREMUREL. 01, Created)
DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)
DT 01-MAR-2003 (TREMUREL. 23, Last annotation update)
DE Barley (H.vulgare) alpha-amylase 2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT "Structure and organization of two divergent alpha-amylase genes from
   RT barley.";
RL Plant Mol. Biol. 9:3-17(1987).
DR EMBL: M17128; AAA32927.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha-amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 438 AA; 47824 MW; 38945AF6DBA2309 CRC64;

Query Match 72.1%; Score 44; DB 10; Length 438;
Best Local Similarity 70.0%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
Db 149 CRDRTKYS DG 158

RESULT 11
O81699 PRELIMINARY; PRT; 434 AA.
AC O81699;
DT 01-NOV-1998 (TREMUREL. 08, Created)
DT 01-NOV-1998 (TREMUREL. 08, Last sequence update)
DT 01-MAR-2003 (TREMUREL. 23, Last annotation update)
DE Alpha amylase precursor (EC 3.2.1.1).
GN ALPHA-AMY2A.
OS Avena fatua.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

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OC Avenae: Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willmott R.L.;
 RL Thesis (1994), University of Bristol.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077315; PubMed-9862499;
 RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
 RT "Dnaei1 footprints suggest the involvement of at least three types of
 transcription factors in the regulation of alpha-Amy2/A by
 gibberellin.";
 RL Plant Mol. Biol. 38:817-825(1998).
 DR EMBL: AJ010728; CAA09323.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase. 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 23
 FT CHAIN 1 434
 SO SEQUENCE 434 AA; 47642 MW; 499F8C3E9767C1E1 CRC64;
 Query Match 68.9%; Score 42; DB 10; Length 434;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CRDDPYADG 10
 Db 148 CRDITYSBG 157
 RESULT 12
 ID 081700 PRELIMINARY; PRT; 437 AA.
 AC 081700;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1).
 GN ALPHA-AMY2D.
 OS Avena fatua.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willmott R.L.;
 RL Thesis (1994), University of Bristol.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99077315; PubMed-9862499;
 RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
 RT "Dnaei1 footprints suggest the involvement of at least three types of
 transcription factors in the regulation of alpha-Amy2/A by
 gibberellin.";
 RL Plant Mol. Biol. 38:817-825(1998).
 DR EMBL: AJ010728; CAA09324.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase. 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 DR SMART: SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 26
 FT CHAIN 1 437
 SO SEQUENCE 437 AA; 47642 MW; 499F8C3E9767C1E1 CRC64;

SO SEQUENCE 437 AA; 48103 MW; 88CE3095737585A CRC64;
 Query Match 68.9%; Score 42; DB 10; Length 437;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CRDDPYADG 10
 Db 151 CRDITYSBG 160
 RESULT 13
 ID 004272 PRELIMINARY; PRT; 278 AA.
 AC 004272;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Chitinase (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrharioideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SRAIN-cv. IR36; TRISUP-leaf;
 RA Yun C.-H., Lee M.-C., Lee J.S., Yun K.J., Eun M.Y.;
 RT "Isolation and characterization of a rice chitinase cDNA clone from
 rice blast fungus-infected rice leaves.";
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF001501; AB58239.1; -.
 DR HSSP: F23951; 2BAA.
 DR Gramene: 004272; -.
 DR InterPro: IPR00726; Glyco_hydro_19.
 DR Pfam: PF00182; Glyco_hydro_19; 1.
 DR ProDom: PD000574; Glyco_hydro_19; 1.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 278 AA; 30721 MW; 9D545C1867915382 CRC64;
 Query Match 67.2%; Score 41; DB 10; Length 278;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 CRDDPYADG 10
 Db 269 CRDQKPYGCG 278
 RESULT 14
 ID 092P43 PRELIMINARY; PRT; 420 AA.
 AC 092P43;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1).
 OS Phaseolus vulgaris (kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosidae;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus;
 OX NCBI_TaxID=3685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mori H.;
 RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mori H., Kobayashi T., Tonokawa T., Tatematsu A., Matsui H.,
 RA Kimura A., Chiba S.;
 RT "Molecular cloning of an alpha-Amylase cDNA from germinating
 cotyledons of kidney bean (Phaseolus vulgaris L. cv. 'Toranabe').";
 J. Appl. Glycosci. 45:261-267(1997).

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DR EMBL: AB015131; BAA33879.1; -.
DR HSPSP; P04063; IAVA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
FT CHAIN 24 420
SQ SEQUENCE 420 AA; 46853 MW; 9A3ECA606C7BB60A CRC64;

Query Match 67.2%; Score 41; DB 10; Length 420;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDRPYADG 10
   1 11 111
Db 146 CKDDTYSDG 155

RESULT 15
ID 042678 PRELIMINARY; PRT; 423 AA.
AC 042678;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha amy1ase precursor (EC 3.2.1.1) (Fragment).
GN CUS AMY2.
OS Cuscuta reflexa (Southern Asian dodder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.
OC Asteridae; Lamiales; Solanales; Convolvulaceae; Cuscuta.
OX NCBI_TaxID=4129;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramachandiran S., Srinivasa B., Mahadevan S.;
RT "Molecular cloning and nucleotide sequence of detachment induced alpha
RT amy1ase from Cuscuta reflexa."
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U06754; AAA16513.1; -.
DR HSPSP; P04063; IAVA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT NON_TER 1 18
FT SIGNAL <1 18
SQ SEQUENCE 423 AA; 46996 MW; 9EF67F8496C2A9F3 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 423;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDRPYADG 10
   1 11 111
Db 143 CKDDTYSDG 152

RESULT 16
ID 08LP27 PRELIMINARY; PRT; 424 AA.
AC 08LP27;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha-amy1ase.
GN PNAMY1.
OS Pharbitis nil (Violet) (Japanese morning glory).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=35883;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-2211127; PubMed-12114559;
RA Nakayama A., Park S., Xu Z., Nakajima M., Yamaguchi I.;
RT "Immunohistochemistry of Active Gibberellins and Gibberellin-Inducible
RT alpha-Amy1ase in Developing Seeds of Morning Glory."
RL Plant Physiol. 129:1045-1053(2002).
DR EMBL: AB077387; BAC02435.1; -.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amy1ase; 1.
DR PRINTS: PR00110; ALPHAMYLASE.
DR SMART: SM00642; Amy; 1.
SQ SEQUENCE 424 AA; 47109 MW; 4CC1FF3733D59742 CRC64;

Query Match 67.2%; Score 41; DB 10; Length 424;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRDDRPYADG 10
   1 11 111
Db 146 CKDDTYSDG 155

RESULT 17
ID 08SX82 PRELIMINARY; PRT; 1593 AA.
AC 08SX82;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE LD15472p (Fragment).
GN UNC-13 OR CG2999.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Berkely;
RC Stapleton M., Brokstein P., Hong L., Agdayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY094789; AAM1142.1; -.
DR FLYBase: FBgn0025726; unc-13.
FT NON_TER 1593 1593
SQ SEQUENCE 1593 AA; 174720 MW; 03450414C0876F38 CRC64;

Query Match 67.2%; Score 41; DB 5; Length 1593;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DDRPYAD 9
   111111111
Db 1305 DDRPYAD 1311

RESULT 18
ID 09V483 PRELIMINARY; PRT; 2871 AA.
AC 09V483;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

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01-MAR-2003 (Tremblrel. 23, last annotation update)
 CG2999 protein.
 UNCL-13 OR CG2999.
 Drosophila melanogaster (Fruit fly).
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 [1]
 SEQUENCE FROM N.A.
 STRAIN-Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer V., Chapple M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borkov D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K.J., Evansgelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbekem C.,
 Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klip D., Lai Z.,
 Lin X., Mattei B., McIntosh T.C., McLeod R.P., McPherson C.,
 Minkler G., Milshina N.V., Mobarry C., Morris J., Mosheiff A.,
 Mount S.M., Moy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195(2000).
 [2]
 SEQUENCE FROM N.A.
 Celniker S.E., Adams M.D., Kronmiller B., Man K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Carlson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 Carlson J.W., Center A., Chapple M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Ferreira S., Frisoe E., Galie R.F., Garg N.S., George R.A.,
 Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 Ibbekem C., Jaitai M., McIntosh T.C., McLeod R.P., McPherson C.,
 McIntosh T.C., Moy M., Murphy B., Nelson C., Pfeiffer B., Pfeiffer A.,
 Paclet J., Paraggs V., Park S., Patel S., Pfeiffer B., Munoo J.,
 Phoumenavong S., Peltman G.S., Puri V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 Seattle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of Drosophila melanogaster genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.
 Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 Ryan J.P., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer V., Chapple M., Pfeiffer B.D.,
 Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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 Lin X., Mattei B., McIntosh T.C., McLeod R.P., McPherson C.,
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 Mount S.M., Moy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L.,
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 Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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 Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
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 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
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 Carlson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
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 Gonzalez M., Houch J., Hoskins R.A., Hostin D., Howland T.J.,
 Ibbekem C., Jaitai M., McIntosh T.C., McLeod R.P., McPherson C.,
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 Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 Mira S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshneft A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Messarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao O.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RP Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferraz S.M., Frisoe E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howard T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshneft A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouaneavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Mistra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn J., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RA Flybase: (SEP-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL: AE003847; AAN06592.1; -
SQ SEQUENCE 2871 AA; 320291 MW; AD88C392C80C89A5 CRC64;
Query Match 67.2%; Score 41; DB 5; Length 2871;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC 08ZE74;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Two-component regulatory system, response regulator protein.
GN RSTB OR YP02308.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Bivolar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagers K., Kariyhev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL: AJ414151; CAC91113.1; -
DR InterPro: IPR001789; Response_reg.
DR InterPro: IPR001867; Trans_reg_C.
DR Pfam: PF00072; Response_reg_1.
DR Pfam: PF00486; Trans_reg_C_1.
DR ProDom: PD000039; Response_reg_1.
DR ProDom: PD000039; Trans_reg_C_1.
DR SMART: SM00448; REC_1.
DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 248 AA; 28023 MW; C857427A4DA796A5 CRC64;
Query Match 65.6%; Score 40; DB 16; Length 248;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 CRDPRPADG 10
Db 64 CRDLRPHYDG 73
RESULT 21
ID 08DOH1 PRELIMINARY; PRT; 266 AA.
AC 08DOH1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Response transcriptional regulatory protein (RstB sensor).
DE RSTB OR Y2139.
GN Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Bivolar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fehreston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nills M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of *Yersinia pestis* KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL: AE013817; AAM85701.1; -
SQ SEQUENCE 266 AA; 30220 MW; F5614BF5C0508F1 CRC64;
Query Match 65.6%; Score 40; DB 16; Length 266;
Best Local Similarity 70.0%; Pred. No. 22;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 CRDPRYADG 10
111 11: 11
DB 82 CRDLRFPHDG 91

RESULT 22

O92RS2 PRELIMINARY; PRT; 405 AA.

AC 092RS2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, last annotation update)
DE Probable glycolate oxidase subunit protein.
GN GICE OR R00778 OR SMC00833.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;

SEQUENCE FROM N.A.

RA STRAIN-1021;
RC MEDLINE-21396507; PubMed-11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boissard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Goffie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maury D.,
RA Pohl T., Portetelle D., Puehler A., Punelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591784; CAC4530.1; -;
DR InterPro: IPR004113; PAD-oxidase.C.
DR InterPro: IPR006094; Oxid.PAD-bind.
DR Pfam: PF01565; PAD-binding_4; 1.
DR Complete proteome.
SQ SEQUENCE 405 AA; 42687 MW; 3060123D124F81EC CRC64;

Query Match 65.6%; Score 40; DB 16; Length 405;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RDDRYADG 10
11: 11111
DB 282 RDDRYADG 290

RESULT 23

O93J13 PRELIMINARY; PRT; 175 AA.

AC 093J13; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Partial putative replication initiator protein (Fragment).
GN SC03995 OR SCBAC2553.32.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;

SEQUENCE FROM N.A.

RA STRAIN-A3(2) / M145;
RC MEDLINE-2196410; PubMed-12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hildalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabbinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL939118; CAC44719.1; -;
KM Complete proteome.
FT NON_TER
SQ SEQUENCE 175 AA; 19485 MW; 2433FA9B15BD7EE8 CRC64;

Query Match 64.8%; Score 39.5; DB 16; Length 175;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CRD-DRPYAD 9
111 11111
DB 61 CRDLDRPYD 70

RESULT 24

O50398 PRELIMINARY; PRT; 144 AA.

AC 050398; 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Hypothetical protein RV3369.
GN RV3369 OR MTW004.27 OR MT3478.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterinae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;

SEQUENCE FROM N.A.

RA STRAIN-H37Rv;
RC MEDLINE-9825987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Barry C.E. III, Tekala F.,
RA Gordon S.V., Eigemeier K., Gas S., Garrier T., Churcher C., Harris D.,
RA Badcock K., Baslam D., Brown D., Chillingworth T., Connor R.,
RA Davies R., DeAngelis K., Felwell T., Gentles S., Hamlin M., Holroyd S.,
RA Hornsby T., Jagels K., Kirogh A., McLean J., Kocula S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).

SEQUENCE FROM N.A.

RA STRAIN-CDC 1551 / Oshkosh;
RC Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Ueberback T., Weidman J., Kouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

EMBL: AL009198; CAAL5754.1; -;

DR EMBL: AE007154; AAK47816.1; -;

DR TIGR: MT3478; -;

DR TubercuList; RV3369; -;

DR Hypothetical protein; Complete proteome.

SQ SEQUENCE 144 AA; 15718 MW; 9102BA411B376DF CRC64;

Query Match 63.9%; Score 39; DB 16; Length 144;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRDPRY 7
1111 11
DB 101 CRDPRY 107

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RESULT 25
Q9A9T6 PRELIMINARY; PRT; 370 AA.
AC Q9A9T6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein CC0876.
GN CC0876.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=153892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nielsen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Ploocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Ueberlack T., Tran K., Wolf A., Vamathevan J., Esmolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005764; AAK2861.1; -.
DR TIGR; CC0876; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 370 AA; 42422 MW; 1D8908EBCBDF357 CRC64;

Query Match 63.9%; Score 39; DB 16; Length 370;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
Db 234 RDDRPRYADG 242

RESULT 26
Q987T8 PRELIMINARY; PRT; 382 AA.
AC Q987T8;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Glycolate oxidase subunits, GICE.
GN MFB6919.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214966;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoto S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003010; BAB53112.1; -.
DR InterPro; IPR004113; FAD-oxidase_C.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF02913; FAD-oxidase_C; 1.
DR Pfam; PF01565; FAD_binding_4; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 40337 MW; 82C9A44BBD0B3475 CRC64;

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Query Match 63.9%; Score 39; DB 16; Length 382;
Best Local Similarity 77.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RDDRPRYADG 10
Db 263 RDDRPRYADG 271

RESULT 27
Q9NGZ3 PRELIMINARY; PRT; 556 AA.
AC Q9NGZ3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Variant-specific surface protein VSP MM/Sac-C/1 (Fragment).
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ad-1;
RA Mansouri M., Ey P.L.;
RT "Analysis of vsp72-like sequences in Giardia intestinalis.";
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF236019; AAF69832.1; -.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR005127; Giardia_VSP.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF03302; VSP; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
FT NON_TER 1
SQ SEQUENCE 556 AA; 57575 MW; F9634BB813863AB6 CRC64;

Query Match 63.9%; Score 39; DB 5; Length 556;
Best Local Similarity 71.4%; Pred. No. 75;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRDDRPY 7
Db 62 CRDDRPY 68

RESULT 28
Q9Y113 PRELIMINARY; PRT; 594 AA.
AC Q9Y113;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE CG12152 protein.
GN BCDNA:GH10353 OR CG12152.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:35:10 ; Search time 30.5714 Seconds
(without alignments)
51.920 Million cell updates/sec

Title: US-09-830-876-3
Perfect score: 56
Sequence: 1 VNMWVKVGS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 56 | 100.0 | 10 | 21 | AAV93373 |
| 2 | 56 | 100.0 | 425 | 21 | AAV93374 |
| 3 | 46 | 82.1 | 435 | 22 | AAV50255 |
| 4 | 46 | 82.1 | 435 | 22 | AAV50255 |
| 5 | 45 | 80.4 | 137 | 21 | AAV61272 |
| 6 | 45 | 80.4 | 428 | 22 | AAV50251 |
| 7 | 45 | 80.4 | 428 | 22 | AAV97245 |
| 8 | 45 | 80.4 | 433 | 15 | AAV51130 |
| 9 | 45 | 80.4 | 434 | 14 | AAV32987 |

| | | | | | | |
|----|----|------|------|----|----------|---------------------|
| 10 | 45 | 80.4 | 434 | 18 | AAV10469 | Rice alpha-amylase |
| 11 | 45 | 80.4 | 434 | 18 | AAV10471 | Rice alpha-amylase |
| 12 | 45 | 80.4 | 434 | 20 | AAV01375 | O sativa alpha-am |
| 13 | 45 | 80.4 | 434 | 20 | AAV81383 | Rice alpha-amylase |
| 14 | 45 | 80.4 | 434 | 21 | AAV72792 | Rice alpha-amylase |
| 15 | 42 | 75.0 | 428 | 21 | AAV12798 | Rice alpha-amylase |
| 16 | 42 | 75.0 | 429 | 16 | AAV6520 | Rice alpha-amylase |
| 17 | 39 | 69.6 | 157 | 23 | AAV8004 | Alpha amylase-7-C |
| 18 | 39 | 69.6 | 548 | 23 | AAV8321 | Listeria monocytog |
| 19 | 38 | 67.9 | 50 | 23 | AAV66859 | Human prostate spe |
| 20 | 38 | 67.9 | 90 | 22 | AAV5532 | Propionibacterium |
| 21 | 38 | 67.9 | 1077 | 23 | AAV74094 | Candida albicans e |
| 22 | 37 | 66.1 | 35 | 22 | AAV62469 | Human immune/haema |
| 23 | 37 | 66.1 | 232 | 23 | AAV6006 | Chlamydia psittaci |
| 24 | 37 | 66.1 | 232 | 23 | AAV62215 | Chlamydia psittaci |
| 25 | 37 | 66.1 | 232 | 23 | AAV62215 | C. psittaci protei |
| 26 | 37 | 66.1 | 527 | 23 | AAV53463 | Lactococcus lactis |
| 27 | 37 | 66.1 | 537 | 20 | AAV88463 | Bacillus agaradhae |
| 28 | 37 | 66.1 | 574 | 17 | AAV00383 | Bacillus cellulase |
| 29 | 37 | 66.1 | 705 | 22 | AAV13298 | Novel human diagno |
| 30 | 37 | 66.1 | 941 | 22 | AAV07095 | Novel human diagno |
| 31 | 37 | 66.1 | 969 | 23 | AAV6007 | Chlamydia psittaci |
| 32 | 37 | 66.1 | 969 | 23 | AAV62215 | C. psittaci protei |
| 33 | 37 | 66.1 | 969 | 23 | AAV62215 | Novel human diagno |
| 34 | 37 | 66.1 | 970 | 22 | AAV6448 | Human immunoglobul |
| 35 | 36 | 64.3 | 63 | 23 | AAV1748 | Human immunoglobul |
| 36 | 36 | 64.3 | 111 | 22 | AAV01762 | Human immunoglobul |
| 37 | 36 | 64.3 | 120 | 22 | AAV48267 | Human immunoglobul |
| 38 | 36 | 64.3 | 137 | 20 | AAV42305 | Human immunoglobul |
| 39 | 36 | 64.3 | 149 | 23 | AAV05783 | Human anti-ganglio |
| 40 | 36 | 64.3 | 341 | 23 | AAV0720 | M. tuberculosis an |
| 41 | 36 | 64.3 | 341 | 23 | AAV0723 | Haemophilus paraga |
| 42 | 36 | 64.3 | 341 | 23 | AAV0726 | Haemophilus paraga |
| 43 | 36 | 64.3 | 341 | 23 | AAV0716 | Haemophilus paraga |
| 44 | 36 | 64.3 | 344 | 23 | AAV0717 | Haemophilus paraga |
| 45 | 36 | 64.3 | 344 | 23 | AAV0718 | Haemophilus paraga |
| 46 | 36 | 64.3 | 344 | 23 | AAV0721 | Haemophilus paraga |
| 47 | 36 | 64.3 | 344 | 23 | AAV0722 | Haemophilus paraga |
| 48 | 36 | 64.3 | 344 | 23 | AAV0724 | Haemophilus paraga |
| 49 | 36 | 64.3 | 344 | 23 | AAV0725 | Haemophilus paraga |
| 50 | 36 | 64.3 | 344 | 23 | AAV0727 | Haemophilus paraga |
| 51 | 36 | 64.3 | 344 | 23 | AAV0728 | Haemophilus paraga |
| 52 | 36 | 64.3 | 348 | 16 | AAV6519 | Alpha amylase-6-C |
| 53 | 36 | 64.3 | 438 | 21 | AAV12797 | Rice alpha-amylase |
| 54 | 36 | 64.3 | 438 | 22 | AAV02850 | Rice alpha-amylase |
| 55 | 36 | 64.3 | 439 | 24 | AAV66633 | Maize alpha-amylase |
| 56 | 36 | 64.3 | 499 | 22 | AAV60481 | Alpha amylase poly |
| 57 | 36 | 64.3 | 499 | 22 | AAV60481 | Drosophila melanog |
| 58 | 36 | 64.3 | 519 | 22 | AAV37465 | Thaumatococcus s |
| 59 | 36 | 64.3 | 536 | 20 | AAV37465 | Chlamydia trachoma |
| 60 | 36 | 64.3 | 550 | 22 | AAV83394 | Salmonella typhi c |
| 61 | 36 | 64.3 | 583 | 21 | AAV45638 | Arabidopsis thalia |
| 62 | 36 | 64.3 | 589 | 21 | AAV30789 | Arabidopsis thalia |
| 63 | 36 | 64.3 | 589 | 21 | AAV30789 | Arabidopsis thalia |
| 64 | 36 | 64.3 | 602 | 21 | AAV45637 | Arabidopsis thalia |
| 65 | 36 | 64.3 | 608 | 21 | AAV45637 | Arabidopsis thalia |
| 66 | 36 | 64.3 | 664 | 23 | AAV81344 | Listeria monocytog |
| 67 | 36 | 64.3 | 664 | 23 | AAV81344 | Agarose 1-7 protei |
| 68 | 35 | 62.5 | 925 | 21 | AAV83735 | zee may protein f |
| 69 | 35 | 62.5 | 47 | 21 | AAV8983 | Human Dps death do |
| 70 | 35 | 62.5 | 101 | 21 | AAV0956 | Human OPRX ORF720 |
| 71 | 35 | 62.5 | 101 | 23 | AAV10801 | Human OPRX protei |
| 72 | 35 | 62.5 | 103 | 22 | AAV0792 | Propionibacterium |
| 73 | 35 | 62.5 | 118 | 22 | AAV02540 | Antil adipocty mon |
| 74 | 35 | 62.5 | 124 | 18 | AAV13533 | Antil melanoma enli |
| 75 | 35 | 62.5 | 132 | 18 | AAV2452 | Mycobacterium tube |
| 76 | 35 | 62.5 | 132 | 18 | AAV2354 | Mycobacterium tube |
| 77 | 35 | 62.5 | 132 | 19 | AAV1657 | M. tuberculosis im |
| 78 | 35 | 62.5 | 132 | 19 | AAV4284 | Mycobacterium tube |
| 79 | 35 | 62.5 | 132 | 20 | AAV3906 | M. tuberculosis an |
| 80 | 35 | 62.5 | 132 | 20 | AAV38959 | M. tuberculosis re |
| 81 | 35 | 62.5 | 132 | 22 | AAV69898 | Mycobacterium tube |
| 82 | 35 | 62.5 | 132 | 22 | AAV69906 | Mycobacterium tube |

| | | | | | | |
|-----|----|------|-----|----|----------|--------------------|
| 83 | 35 | 62.5 | 132 | 22 | AA01253 | Mycobacterium tube |
| 84 | 35 | 62.5 | 132 | 22 | AA01261 | Mycobacterium tube |
| 85 | 35 | 62.5 | 132 | 22 | AA001889 | M. tuberculosis pa |
| 86 | 35 | 62.5 | 132 | 23 | AAE29705 | Mycobacterium tube |
| 87 | 35 | 62.5 | 132 | 23 | ABR95358 | M tuberculosis ant |
| 88 | 35 | 62.5 | 132 | 23 | ABR95366 | M tuberculosis ant |
| 89 | 35 | 62.5 | 132 | 23 | AAE17569 | Mycobacterium spec |
| 90 | 35 | 62.5 | 132 | 24 | ABU71789 | Prostate cancer as |
| 91 | 35 | 62.5 | 132 | 24 | ABU71797 | Prostate cancer as |
| 92 | 35 | 62.5 | 180 | 22 | AA081997 | Human haematologic |
| 93 | 35 | 62.5 | 264 | 23 | ABP30446 | Streptococcus poly |
| 94 | 35 | 62.5 | 290 | 23 | ABP27789 | Streptococcus poly |
| 95 | 35 | 62.5 | 303 | 19 | AA076828 | Human TR6 partial |
| 96 | 35 | 62.5 | 303 | 22 | AA084849 | Partial amino acid |
| 97 | 35 | 62.5 | 318 | 22 | AA090956 | C glutamicum prote |
| 98 | 35 | 62.5 | 327 | 23 | ABR80571 | Human sb9614126com |
| 99 | 35 | 62.5 | 355 | 18 | AA032435 | Mycobacterium tube |
| 100 | 35 | 62.5 | 355 | 18 | AA032367 | Mycobacterium tube |

ALIGNMENTS

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RESULT 1
AA093373
ID AA093373 standard; peptide: 10 AA.
AC AA093373;
XX
DT 04-SEP-2000 (first entry)
DE Amino acid sequence of an epitope of the wheat alpha-amylase.
XX
KW Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;
KW cereal grain.
XX
OS Triticum aestivum.
XX
PN WO200028319-A1.
XX
PD 18-MAY-2000.
XX
PE 11-NOV-1999; 99WO-AU00995.
XX
PR 11-NOV-1998; 98AU-0007058.
XX
PA (QUAL-) QUALITY WHEAT CRC LTD.
XX
PI Skeritt JH;
XX
DR WPI: 2000-376655/32.
XX
PT Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -
XX
XX
XX Claim 1; Page 29; 52pp; English.
XX
XX The present sequence represents an epitope from the wheat alpha-amylase.
XX Antibodies which recognise the epitope are used in a two-site
XX immunoassay for qualitative or quantitative detection of alpha-amylase
XX in a test sample. The assay is used for detecting weather damage in a
XX cereal grain. Weather damage is caused by the action of hydrolytic
XX enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate
XX the breakdown of starch granules and protein in the endosperm of
XX germinating grain. Individual growers can identify areas of sprouting
XX prior to harvest, preventing contamination of sound wheat by weather
XX damaged wheat. The damaged grain can be harvested separately from the
XX sound grain and financial losses resulting from down grading the whole
XX crop can be avoided. The two-site immunoassays can be applied at mill
XX or silo (elevator) receipt of grain or can be used on farms with minimal
XX equipment requirements.

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SQ Sequence 10 AA;
Query Match 100.0%; Score 56; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VNMVNVKVGGS 10
DB 1 VNMVNVKVGGS 10

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RESULT 2
AA093374
ID AA093374 standard; protein: 425 AA.
AC AA093374;
XX
DT 04-SEP-2000 (first entry)
DE Amino acid sequence a wheat alpha-amylase.
XX
KW Epitope: wheat; alpha-amylase; two-site immunoassay; weather damage;
KW cereal grain.
XX
OS Triticum aestivum.
XX
PN WO200028319-A1.
XX
PD 18-MAY-2000.
XX
PE 11-NOV-1999; 99WO-AU00995.
XX
PR 11-NOV-1998; 98AU-0007058.
XX
PA (QUAL-) QUALITY WHEAT CRC LTD.
XX
PI Skeritt JH;
XX
DR WPI: 2000-376655/32.
XX
PT Two site immunoassay for the qualitative or quantitative detection of
PT alpha-amylase in a test sample, used to detect weather damage in a
PT cereal grain, such as wheat, rye, triticale or barley -
XX
XX
XX Disclosure; Fig 3; 52pp; English.
XX
XX The present sequence represents a wheat alpha-amylase. Antibodies
XX which recognise epitopes from this protein are used in a two-site
XX immunoassay for qualitative or quantitative detection of alpha-amylase
XX in a test sample. The assay is used for detecting weather damage in a
XX cereal grain. Weather damage is caused by the action of hydrolytic
XX enzymes, e.g. amylases, in the grain endosperm. These enzymes accelerate
XX the breakdown of starch granules and protein in the endosperm of
XX germinating grain. Individual growers can identify areas of sprouting
XX prior to harvest, preventing contamination of sound wheat by weather
XX damaged wheat. The damaged grain can be harvested separately from the
XX sound grain and financial losses resulting from down grading the whole
XX crop can be avoided. The two-site immunoassays can be applied at mill
XX or silo (elevator) receipt of grain or can be used on farms with minimal
XX equipment requirements.
SQ Sequence 425 AA;
Query Match 100.0%; Score 56; DB 21; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VNMVNVKVGGS 10
DB 251 VNMVNVKVGGS 260

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RESULT 3

AAM50253
 ID AAM50253 standard; Protein: 435 AA.
 AC AAM50253;
 XX
 XX 21-JAN-2002 (first entry)
 DE Rice alpha-amylase (alpha-Amy3-C gene product).
 XX Alpha-amylase; promoter; rice; transgenic plant; angiosperm;
 KW monocot; cereal; brewing.
 XX
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Signal_peptide
 FT 26..428
 FT /label= Mature_protein
 XX
 PM US6288302-B1.
 XX
 PD 11-SEP-2001.
 XX
 PF 04-MAY-1998; 98US-0072917.
 XX
 PR 04-NOV-1992; 92US-0973324.
 PR 01-AUG-1995; 95US-0509962.
 PR 08-OCT-1997; 97US-0947201.
 PR 22-NOV-1994; 94US-0343380.
 XX
 PA (NASC-) NAT SCI COUNCIL ROC.
 XX
 PI Yu S, Liu L, Chan M;
 XX
 DR WPI: 2001-647191/74.
 DR N-PSDB; AAT70540.
 XX
 PT Producing a transgenic monocot plant comprising a transgene under
 PT control of an alpha amylase promoter and signal peptide sequences,
 PT provides transgenic plants particularly cereals for the brewing
 PT industry -
 XX
 PS Disclosure: Column 79-82; 44pp; English.
 XX
 CC The present sequence is that of alpha-amylase encoded by DNA clone
 CC alpha-Amy3-C (see AAT70540). Expression of alpha-Amy3-C increases
 CC 5-fold following sugar starvation. The invention relates to
 CC the use of an alpha-amylase gene promoter and signal sequence in
 CC the production of recombinant proteins in transgenic plants and
 CC transgenic plant seeds. In a claimed method, a transgenic monocot
 CC is obtained by: transforming an immature embryo of the plant via
 CC Agrobacterium-mediated transformation with DNA comprising a plant
 CC alpha-amylase promoter (e.g. the rice alpha-Amy3-C promoter) that
 CC is induced under sugar-depleted or sugar-free conditions, a signal
 CC peptide sequence, and an exogenous sequence encoding a gene product;
 CC regenerating the transformed plant; and growing the transgenic
 CC plant, which expresses the gene product under sugar-depleted or
 CC sugar-free conditions. The gene product may also be obtained by
 CC culturing an angiosperm host cell. The transgenic monocot plants
 CC are especially useful in brewing and to produce glucose from starch.
 XX
 SQ Sequence 435 AA;
 Query Match 82.1%; Score 46; DB 22; Length 435;
 Best Local Similarity 88.9%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VNMVNRVGG 9
 DB 253 VNMVNAVGG 261

RESULT 4
 AAB97247
 ID AAB97247 standard; Protein: 435 AA.
 AC AAB97247;
 XX
 XX 31-JUL-2001 (first entry)
 DE Alpha-amylase related protein #3.
 XX Alpha-amylase; promoter; expression vector; rice.
 KW
 XX
 OS Unidentified.
 XX
 PN TW402638-A.
 XX
 PD 21-AUG-2000.
 XX
 PF 13-FEB-1992; 97TW-0101436.
 XX
 PR 13-FEB-1992; 97TW-0101436.
 XX
 PA (NASC-) NAT SCI COUNCIL.
 XX
 PI Yu S, Liou L;
 XX
 DR WPI: 2001-167365/17.
 DR N-PSDB; AAH20285.
 XX
 PT Gene expression system comprising the promoter region of alpha-amylase
 PT gene, produces large quantities of alpha-amylase in culture medium of
 PT sugar starved rice -
 XX
 PS Disclosure; Fig 12; 104pp; Chinese.
 XX
 CC This invention relates to a gene expression system comprising the
 CC alpha-amylase gene promoter DNA encoding the signal peptide of
 CC alpha-amylase and the promoter along with the glucanase reporter gene
 CC and hygromycin resistance gene are used in the construction of a GUS gene
 CC expression vector, which when transformed into rice suspension-cultured
 CC cells, can be used to investigate the expression of the vector under the
 CC control of the promoter. The gene expression system can be used to
 CC conduct gene regulation and protein expression and secretion using the
 CC characteristics of the alpha-amylase gene promoter and the DNA sequence
 CC encoding the signal peptide. The present sequence represents an
 CC alpha-amylase related protein used in the course of the present
 CC invention.
 XX
 SQ Sequence 435 AA;
 Query Match 82.1%; Score 46; DB 22; Length 435;
 Best Local Similarity 88.9%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VNMVNRVGG 9
 DB 253 VNMVNAVGG 261
 RESULT 5
 AAB16272
 ID AAB16272 standard; Protein: 157 AA.
 AC AAB16272;
 XX
 XX 31-OCT-2000 (first entry)
 DE Pinus radiata amylase protein sequence SEQ ID NO:34.
 XX
 KW Eucalyptus grandis; pinus radiata; Monterey pine; modification;
 KW plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
 KW transgenic plant.
 XX

[illegible]

| | | | |
|-----------------------|---|---------------|----------------------|
| XX | 04-MAY-1998; | 98US-0072917. | |
| PF | | | |
| XX | 04-NOV-1992; | 92US-0973324. | |
| PR | 01-AUG-1995; | 95US-0509962. | |
| PR | 08-OCT-1997; | 97US-0947201. | |
| XX | 22-NOV-1994; | 94US-0343380. | |
| PA | (NASC-) NAT SCI COUNCIL ROC. | | |
| XX | | | |
| PI | Yu S, Liu L, Chan M; | | |
| XX | | | |
| DR | WPI; 2001-647191/74. | | |
| DR | N-PSDB; AAI70537. | | |
| XX | | | |
| PT | Producing a transgenic monocot plant comprising a transgene under | | |
| PT | control of an alpha amylase promoter and signal peptide sequences, | | |
| PT | provides transgenic plants particularly cereals for the brewing | | |
| XX | industry | | |
| XX | | | |
| PS | Example 1: Column 61-64; 44pp; English. | | |
| CC | | | |
| CC | The present sequence is that of rice (<i>Oryza sativa</i>) cv. M202 | | |
| CC | alpha-amylase, encoded by isolated genomic DNA clone alpha-Amy7-C | | |
| CC | (see AAI70537). Expression of alpha-Amy7-C in cultured suspension | | |
| CC | cells of rice was induced 6-fold at day 12 after sugar depletion, | | |
| CC | and continued to increase up to day 14. The invention relates to | | |
| CC | the use of an alpha-amylase gene promoter and signal sequence in | | |
| CC | the production of recombinant proteins in transgenic plants and | | |
| CC | transgenic plant seeds. In a claimed method, a transgenic monocot | | |
| CC | is obtained by: transforming an immature embryo of the plant via | | |
| CC | Agrobacterium-mediated transformation with DNA comprising a plant | | |
| CC | alpha-amylase promoter (e.g. the rice alpha-Amy7-C promoter) that | | |
| CC | is induced under sugar-depleted or sugar-free conditions, a signal | | |
| CC | peptide sequence, and an exogenous sequence encoding a gene product; | | |
| CC | regenerating the transformed plant; and growing the transgenic | | |
| CC | plant, which expresses the gene product under sugar-depleted or | | |
| CC | sugar-free conditions. The gene product may also be obtained by | | |
| CC | cultivating an angiosperm host cell. The transgenic monocot plants | | |
| CC | are especially useful in brewing and to produce glucose from starch. | | |
| XX | | | |
| XX | Sequence | 428 AA; | |
| SO | | | |
| Query Match | 80.4%; | Score 45; | DB 22; Length 428; |
| Best Local Similarity | 70.0%; | Fred. No. 20; | |
| Matches | 7; Conservative | 3; Mismatches | 0; Indels 0; Gaps 0; |
| QY | 1 VNMVTKVGS 10 | | |
| | :: | | |
| DB | 253 VNMWDRVGA 262 | | |
| RESULT 7 | | | |
| AAB97245 | | | |
| ID | AAB97245 standard; Protein; 428 AA. | | |
| XX | | | |
| AC | AAB97245; | | |
| XX | | | |
| DT | 31-JUL-2001 (first entry) | | |
| XX | | | |
| DE | Alpha-amylase related protein #1. | | |
| XX | | | |
| KW | Alpha-amylase; promoter; expression vector; rice. | | |
| XX | | | |
| OS | Unidentified. | | |
| XX | | | |
| PN | TW402638-A. | | |
| XX | | | |
| PD | 21-AUG-2000. | | |
| XX | | | |
| PF | 13-FEB-1992; 97TW-0101436. | | |
| XX | | | |
| PR | 13-FEB-1992; 97TW-0101436. | | |

XX (NASC-) NAT SCI COUNCIL.
 XX Yu S, Liou L;
 XX WPI: 2001-167365/17.
 DR N-PSDB; AAH20283.
 XX
 PT Gene expression system comprising the promoter region of alpha-amylase
 PT gene, produces large quantities of alpha-amylase in culture medium of
 PT sugar starved rice -
 XX
 PS Disclosure: Fig 8; 104pp; Chinese.
 XX
 CC This invention relates to a gene expression system comprising the
 CC alpha-amylase gene promoter, DNA encoding the signal peptide of
 CC alpha-amylase and the promoter along with the glucuronidase reporter gene
 CC and hygromycin resistance gene are used in the construction of a GUS gene
 CC expression vector, which when transformed into rice suspension-cultured
 CC cells, can be used to investigate the expression of the vector under the
 CC control of the promoter. The gene expression system can be used to
 CC conduct gene regulation and protein expression and secretion using the
 CC characteristics of the alpha-amylase gene promoter and the DNA sequence
 CC encoding the signal peptide. The present sequence represents an
 CC alpha-amylase related protein used in the course of the present
 CC invention.
 CC
 XX Sequence 428 AA;
 SQ
 Query Match 80.4%; Score 45; DB 22; Length 428;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNWNKVGCS 10
 ||||:||||
 Db 253 VNWDVGVGA 262
 RESULT 8
 ID AAR55130 standard; Protein: 433 AA.
 XX AAR55130;
 AC AAR55130;
 XX
 DT 25-MAR-2003 (updated)
 DT 12-JUN-1995 (first entry)
 XX
 DE Rice alpha-amylase coding.
 XX
 KM Virus: recombination; plant virus; alpha trichosanthin; phenotype;
 KM alpha amylase; alpha haemoglobin; brome mosaic virus; gemini virus;
 KM rice necrosis virus tobamovirus; gene expression; chinese cucumber.
 XX
 OS Oryza sativa.
 XX
 PN US5316931-A.
 XX
 PD 31-MAY-1994.
 XX
 PF 31-JUL-1992; 92US-0923692.
 XX
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 22-OCT-1990; 90US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737699.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (BIOS-) BIOSOURCE GENETICS CORP.

XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grille LK;
 PI Turpen AM, Turpen TH;
 XX WPI: 1994-176269/21.
 DR N-PSDB; AAO65574.
 XX
 PT New recombinant plant viral nucleic acid - capable of systemic
 PT infection and stable expression of non-native nucleic acid in
 PT plant host
 XX
 PS Example 4; Columns 53-56; 44pp; English.
 XX
 CC The rice alpha-amylase gene may be inserted into a recombinant plant
 CC virus which can then be used to infect plants for the production of
 CC non-native products (in this case alpha-amylase). Other genes which
 CC may be inserted into the virus are those which control a phenotypic
 CC trait, such as male sterility, or sequences encoding anti-sense RNA
 CC which can be useful to prevent the expression of undesired phenotypic
 CC traits. The recombinant virus is derived from a plus sense, single
 CC stranded virus selected from tobamovirus, brome mosaic virus, rice
 CC necrosis virus or a gemini virus.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX Sequence 433 AA;
 SQ
 Query Match 80.4%; Score 45; DB 15; Length 433;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNWNKVGCS 10
 ||||:||||
 Db 258 VNWDVGVGA 267
 RESULT 9
 ID AAR32987 standard; Protein: 434 AA.
 XX AAR32987;
 AC AAR32987;
 XX
 DT 25-MAR-2003 (updated)
 DT 17-JUN-1993 (first entry)
 XX
 DE Rice alpha-amylase.
 XX
 KM Recombinant products; commercial production; fermentation;
 KM diosynthesist; natural products; recombinant proteins;
 KM product expression; protein expression; expressed proteins.
 XX
 OS Oryza sativa.
 XX
 PN WO9303161-A1.
 XX
 PD 18-FEB-1993.
 XX
 PF 31-JUL-1992; 92WO-US06359.
 XX
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (DAMS/) DAWSON W O.
 PA (DONS/) DONSON J.
 PA (GARG/) GARGER S J.
 PA (GRAN/) GRANTHAM G L.
 PA (GRIL/) GRILLE L K.
 PA (TURP/) TURPEN A M.
 PA (TURP/) TURPEN T H.
 XX
 PI Donson J, Dawson WO, Grantham GL, Turpen TH, Turpen AM, Garger SJ;
 PI Grille LK.
 XX WPI: 1993-076518/09.
 DR N-PSDB; AAO37680.

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XX Recombinant plant viral nucleic acids - used to express a prod.,
PT e.g. antibody or IL-1 in a plant
XX
XX Example 4; Page 96; 30pp; English.
PS
XX This sequence is rice alpha amylase. The coding sequence was inserted
CC into a recombinant plant viral nucleic acid which was then used to
CC express a recombinant product (in this case rice alpha-amylase) in a
CC plant. The plant viral sequence may be from tobacco mosaic, cucumber
CC green mottle, cowpea mosaic, bromo mosaic, broad bean mottle, rice
CC necrosis, geminiviruses, tomato golden mosaic, Cassava latent and
CC maize streak viruses.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
CC
XX Sequence 434 AA;
SO
Query Match 80.4%; Score 45; DB 14; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VNMVNVKVGGS 10
    ||||:||||:
Db 259 VNMVDRVGA 268
RESULT 10
AAW10469
ID AAW10469 standard; Protein: 434 AA.
XX
XX AAW10469;
AC
XX 26-APR-1997 (first entry)
DT
XX
XX Rice alpha-amylase.
DE
XX
XX Recombinant viral nucleic acid; RNA virus; vector;
KM tobacco mosaic virus; TMV; rice; alpha-amylase; transgenic plant.
KW
XX
XX Oryza sativa.
OS
XX
XX WO9640867-A1.
PN
XX
XX 19-DEC-1996.
PD
XX
XX 06-JUN-1996; 96WO-US09299.
PF
XX
XX 07-JUN-1995; 95US-0483502.
PR
XX
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
PA
XX
XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
DR WPI: 1997-065181/06.
XX
XX N-PSDB; AAT47095.
DR
XX
XX Recombinant viral nucleic acid producing, e.g. male sterility in
PT plants - comprises nucleic acid whose transcription is controlled by
PT another sequence
XX
XX Example 4; Page 127-129; 149pp; English.
PS
XX A DNA sequence (AAT47095) codes for rice alpha-amylase (AAW10469).
CC Novel viral nucleic acids can be constructed in which the alpha-
CC amylase coding sequence is placed under control of the promoter
CC of the tobacco mosaic virus coat protein gene, which has been
CC deleted. The recombinant viral nucleic acid is capable of self-
CC replication, encapsidation and systemic spread in infected tobacco
CC plants, and directs expression of the alpha-amylase in plant
CC tissue.
XX

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SQ Sequence 434 AA;
Query Match 80.4%; Score 45; DB 18; Length 434;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VNMVNVKVGGS 10
    ||||:||||:
Db 259 VNMVDRVGA 268
RESULT 11
AAW11871
ID AAW11871 standard; Protein: 434 AA.
XX
XX AAW11871;
AC
XX 25-MAR-2003 (updated)
DT 21-APR-1997 (first entry)
DT
XX
XX Rice alpha-amylase.
DE
XX
XX Recombinant virus; alpha-haemoglobin; human; chinese cucumber;
KM alpha-trichosanthin; rice; alpha amylase; beta-haemoglobin;
KW subgenomic promoter; coat protein.
XX
XX Oryza sativa.
OS
XX
XX US5589367-A.
PN
XX
XX 31-DEC-1996.
PD
XX
XX 19-JAN-1994; 94US-0184237.
PF
XX
XX 17-FEB-1989; 89US-0310881.
PR 05-MAY-1989; 89US-0347637.
PR 08-JUN-1989; 89US-0363138.
PR 31-JUL-1992; 92US-0923692.
PR 26-FEB-1988; 88US-0160766.
PR 26-FEB-1988; 88US-0160771.
PR 15-JUL-1988; 88US-0219279.
PR 22-OCT-1990; 90US-0600244.
PR 16-JAN-1991; 91US-0641617.
PR 26-JUL-1991; 91US-0737899.
PR 01-AUG-1991; 91US-0739143.
XX
XX (BIOS-) BIOSOURCE TECHNOLOGIES INC.
PA
XX
XX Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
PI Turpen AM, Turpen TH;
DR WPI: 1997-076845/07.
XX
XX N-PSDB; AAT61377.
DR
XX
XX Recombinant viral DNA for altering plant phenotype or protein prodn
PT - contains non-native sub-genomic promoter for expression of
PT heterologous protein and native promoter for expression of coat
PT protein
XX
XX Example 4; Column 49-52; 42pp; English.
PS
XX The sequences given in AAW11868-71 represent proteins which were
CC produced by the recombinant viruses of the invention. The
CC viruses are recombinant plant viruses which comprise a native plant
CC virus subgenomic promoter, at least one non-native plant virus
CC subgenomic promoter, and a sequence encoding a plant virus coat
CC protein. These heterologous sequences are preferably under the
CC control of the native promoter sequence. By using a plant virus
CC existing cells can be altered with a new coding sequences without
CC involving germ cell. The recombinant viruses are stable and can
CC cause systemic infection, with stable expression/transcription in
CC plants that are hosts for the non-native part of the vector. The
CC nucleotide sequences encoding these protein preferably integrated
XX

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in plant viruses having either the O-coat protein or the U1-coat protein gene.
 CC (updated on 25-MAR-2003 to correct PF field.)
 CC (updated on 25-MAR-2003 to correct PR field.)
 CC
 XX Sequence 434 AA;
 SQ
 Query Match 80.4%; Score 45; DB 18; Length 434;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVNRVGG 10
 DB 259 VNMVDRVGA 268
 RESULT 12
 ID AAY01375 standard; Protein: 434 AA.
 AC AAY01375;
 XX 20-MAR-2003 (updated)
 DT 04-JUN-1999 (first entry)
 XX
 DE O. sativa alpha-amylase.
 KW Recombinant; plant virus; coat protein; systemic infection;
 KM transcription; therapeutic; rice; alpha-amylase.
 OS Oryza sativa.
 XX
 PN US5889190-A.
 PD 30-MAR-1999.
 XX
 PF 07-JUN-1995; 95US-0480432.
 XX
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 31-JUL-1992; 92US-0923592.
 PR 12-JUN-1992; 92US-0184237.
 PR 26-FEB-1988; 88US-0160766.
 PR 26-FEB-1988; 88US-0160771.
 PR 15-JUL-1988; 88US-0219279.
 PR 22-OCT-1990; 91US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1999-243290/20.
 DR N-PSDB; AAX29144.
 XX
 PT Recombinant plant viral nucleic acid derived from a plus sense,
 PT single stranded RNA plant virus - useful for the transcription of
 PT products in a host
 XX
 PS Example 4: Columns 47-51; 46pp; English.
 XX
 CC The invention relates to a recombinant plant viral nucleic acid derived
 CC from a plus sense, single stranded RNA plant virus. The recombinant plant
 CC viral nucleic acid comprises: (a) a first plant viral subgenomic promoter
 CC that is native to the plus sense, single stranded RNA plant virus and
 CC operably joined to a first nucleic acid expression sequence; and (b) a
 CC second plant viral subgenomic promoter that is non-native and is operably
 CC joined to a second nucleic acid expression sequence; where, (i) (a) and
 CC (b) are incapable of recombination with one another, (ii) either the

first or the second nucleic acid expression sequence is a plant viral
 CC coat protein coding sequence. The recombinant plant viral nucleic acid
 CC allows the transcription of products in a host, such as therapeutic and
 CC other useful polypeptides or proteins e.g. enzymes, complex biomolecules
 CC and ribozymes. It also gives the option of applying the coding sequence
 CC to the desired organism, tissue, organ or cell, is stable for the foreign
 CC coding sequences and is capable of systemic infection in the plant host.
 CC The transformation and regeneration of target organisms become
 CC unnecessary.
 CC (updated on 20-MAR-2003 to correct PR field.)
 CC
 XX Sequence 434 AA;
 SQ
 Query Match 80.4%; Score 45; DB 20; Length 434;
 Best Local Similarity 70.0%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VNMVNRVGG 10
 DB 259 VNMVDRVGA 268
 RESULT 13
 ID AAM84383 standard; Protein: 434 AA.
 AC AAM84383;
 XX 01-APR-1999 (first entry)
 DT
 XX
 DE Rice alpha-amylase sequence.
 XX
 KW Rice; alpha-amylase; plant virus; RNA plant virus promoter;
 KM systemic infection; foreign gene expression; AIDS therapeutic drug.
 XX
 OS Oryza sativa.
 XX
 PN US5866785-A.
 PD 02-FEB-1999.
 XX
 PF 07-JUN-1995; 95US-0482920.
 XX
 PR 31-JUL-1992; 92US-0923692.
 PR 26-FEB-1988; 88US-0160766.
 PR 15-JUL-1988; 88US-0219279.
 PR 17-FEB-1989; 89US-0310881.
 PR 05-MAY-1989; 89US-0347637.
 PR 08-JUN-1989; 89US-0363138.
 PR 22-OCT-1990; 91US-0600244.
 PR 16-JAN-1991; 91US-0641617.
 PR 26-JUL-1991; 91US-0737899.
 PR 01-AUG-1991; 91US-0739143.
 PR 19-JAN-1994; 94US-0184237.
 PR 07-JUN-1995; 95US-0482920.
 XX
 PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.
 XX
 PI Dawson WO, Donson J, Garger SJ, Grantham GL, Grill LK;
 PI Turpen AM, Turpen TH;
 XX
 DR WPI: 1999-142035/12.
 DR N-PSDB; AAX03386.
 XX
 PT Recombinant plant viral vector - that is capable of systemic
 PT infection in host plant and stable production of heterologous DNA
 PT useful for producing therapeutic proteins for treating e.g. AIDS
 XX
 PS Example 4: Columns 51-54; 45pp; English.
 XX
 CC The present sequence represents rice alpha-amylase. The nucleic
 CC acid sequence can be expressed in the plant viral constructs of the

CC invention. The specification describes a recombinant plant viral
CC nucleic acid derived from a positive (+)-sense RNA plant virus comprising
CC a native (+)-sense RNA plant virus promoter that is linked to an
CC expression sequence and a heterologous (+)-sense RNA plant virus
CC promoter that is linked to an expression sequence. The promoters are
CC incapable of recombination with each other, and one of the expression
CC sequences encodes a plant viral coat protein while the other is
CC optionally a heterologous coding sequence. The plant viral nucleic acid
CC is capable of systemic infection in a host plant. The viral construct is
CC useful for the introduction and expression of non-viral foreign genes
CC in plants and the production of e.g. potential AIDS therapeutic drugs.

SO Sequence 434 AA;

Query Match 80.4%; Score 45; DB 20; Length 434;

Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNWNKRYGGS 10
DB 259 VNWVDRVGGA 268
|||||:||||

RESULT 14

ID AAY87792 standard; Protein: 434 AA.

AC AAY87792;

DT 24-AUG-2000 (first entry)

DE Rice alpha-amylase protein.

KM Animal RNA virus; viral coat protein; plant; male sterility;

KW Interleukin; EPO; erythropoietin; CSF; colony stimulating factor;

KM Factor VIII; hGH; human growth hormone; melanin; insulin; vaccine;

KW stereo specific catalysis; alpha-amylase; rice.

OS Oryza sativa.

PN US6054566-A.

PD 25-APR-2000.

PE 07-JUN-1995; 9505-0484341.

PF 17-FEB-1989; 89US-0310881.

PR 08-JUN-1989; 89US-0363138.

PR 26-FEB-1988; 88US-0160766.

PR 26-FEB-1988; 88US-0160771.

PR 15-JUL-1988; 88US-0219279.

PR 05-MAY-1989; 89US-0347637.

PR 22-OCT-1990; 90US-0600244.

PR 16-JAN-1991; 91US-0641617.

PR 26-JUL-1991; 91US-0737899.

PR 01-AUG-1991; 91US-0739143.

PR 31-JUL-1992; 92US-0923692.

PA (BIOS-) BIOSOURCE TECHNOLOGIES INC.

PI Garger SJ, Grill LK, Turpen TH, Grantham GL, Dawson WO, Turpen AM;
PI Donson J;

XX WPI: 2000-338510/29.

XX N-PSDB; AAA12394.

XX Recombinant non-retroviral nucleic acid for producing proteins such as
XX Interleukins, melanin and vaccines, comprises subgenomic promoters
XX linked to sequences coding for viral coat protein and heterologous
XX proteins -
XX Example 4; Column 65-68; 51pp; English.

CC This invention describes a novel recombinant viral nucleic acid (I)
CC from a non-retroviral (+) sense, single stranded animal RNA virus
CC comprising a nucleic acid sequence coding for a viral coat protein
CC regulated by a native subgenomic promoter and other two heterologous
CC nucleic acid sequences regulated by two other subgenomic promoters.
CC (I) is useful for expressing foreign genes e.g. genes inducing male
CC sterility in plants. (I) is also useful for producing proteins such as
CC Interleukins, EPO (erythropoietin), CSF (colony stimulating factor),
CC Factor VIII, hGH (human growth hormone), melanin, insulin, vaccines
CC etc., and enzymes that are useful for stereo specific catalysis of
CC organic compounds. (I) is stable and transcribed systemically. The dual
CC subgenomic promoter system reduces the frequency of recombination thus
CC reducing regeneration of the wild type virus. This sequence represents
CC a rice alpha-amylase protein which is described in the method of the
CC invention.

SO Sequence 434 AA;

Query Match 80.4%; Score 45; DB 21; Length 434;

Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNWNKRYGGS 10
DB 259 VNWVDRVGGA 268
|||||:||||

RESULT 15

ID AAB12798 standard; Protein: 428 AA.

AC AAB12798;

DT 23-NOV-2000 (first entry)

DE Rice alpha-Amy7-C protein seq ID NO:2.

KM Rice; alpha-Amy6-C; alpha-Amy7-C; alpha-Amy8-C; alpha-Amy10-C;

KW gene expression; promoter region; alpha-amylase; transgenic plant.

OS Oryza sativa.

PN JP2000157080-A.

PD 13-JUN-2000.

PE 04-NOV-1993; 99JP-0356560.

PR 05-NOV-1992; 92JP-0321274.

PR 04-NOV-1993; 93JP-0297607.

PA (NASC-) NAT SCI COUNCIL.

DR WPI: 2000-468171/41.

DR N-PSDB; AAA72947.

PT A gene expression system containing the promoter region of
PT alpha-amylase gene, useful for mass production of a desired gene
PT product in a plant host cell

XX Example 1; Page 27-30; 39pp; Japanese.

XX The present invention describes a gene expression system containing the
XX promoter region of an alpha-amylase gene. Also described is a method for
XX preparing a transgenic rice plant comprising: (1) infecting Agrobacterium
XX into an unmatred embryo of a rice plant; (2) simultaneously culturing
XX the embryo with a suspended culture of a dicotyledon during the
XX transforming step; (3) growing the transformed embryo to a callus in a
XX selective medium containing a plant growth hormone; and (4) regenerating
XX the callus to roots and sprouts in a regeneration medium. The method can
XX be used for mass production of a desired gene product in a plant host
XX cell. The present sequence represents the rice alpha-Amy7-C protein,
XX which is used in an example from the present invention.

| XX | Sequence | 428 AA; | 75.0%; Score 42; | DB 21; | Length 428; |
|-----------|--|--------------------------------|------------------|---------------|----------------------|
| XX | Query Match | | 70.0%; | Pred. No. 62; | |
| XX | Best local similarity | | 70.0%; | Mismatches | 1; Indels 0; Gaps 0; |
| XX | Matches | 7; Conservative | 2; | Mismatches | 1; Indels 0; Gaps 0; |
| OY | 1 VNNVNVVGGG 10 | : | | | |
| DB | 253 VNNVDHVGGA 262 | | | | |
| RESULT 16 | | | | | |
| AAAR76520 | AAAR76520 standard; Protein; 429 AA. | | | | |
| AC | AAAR76520; | | | | |
| XX | 14-FEB-1996 (first entry) | | | | |
| XX | Alpha-amylase-7-C. | | | | |
| XX | Alpha-Amy-6-C; amylase; promoter; vector; heterologous; | | | | |
| KM | gene expression system. | | | | |
| XX | Oryzae sativa. | | | | |
| OS | | | | | |
| XX | Key | Location/Qualifiers | | | |
| FT | Misc-difference 35 | /note= "corresp. to GAC codon" | | | |
| FT | Misc-difference 83 | /note= "corresp. to CAG codon" | | | |
| FT | Misc-difference 158 | /note= "corresp. to CAG codon" | | | |
| FT | Misc-difference 218 | /note= "corresp. to GAC codon" | | | |
| FT | Misc-difference 224 | /note= "corresp. to TAC codon" | | | |
| FT | Misc-difference 233 | /note= "corresp. to CGG codon" | | | |
| FT | Misc-difference 233 | /note= "corresp. to CGT codon" | | | |
| FT | Misc-difference 294 | /note= "corresp. to CAG codon" | | | |
| FN | JP07143895-A. | | | | |
| XX | 06-JUN-1995. | | | | |
| XX | 04-NOV-1993; | 93JP-0297607. | | | |
| XX | 05-NOV-1992; | 92JP-0321274. | | | |
| XX | (NASC-) NAT SCI COUNCIL. | | | | |
| XX | WPI; 1995-236472/31. | | | | |
| XX | N-PSDB; AAO92806. | | | | |
| XX | Gene expression system contg. alpha-amylase gene promoter - for use | | | | |
| XX | in plants for expression of heterologous genes | | | | |
| XX | Claim 3; Page 27-30; 42pp; Japanese. | | | | |
| XX | AAAR76519-P76521 represent the amylase gene products alpha-amylase-6-C, | | | | |
| XX | alpha-amylase-7-C and alpha-amylase-8-C respectively. The promoter | | | | |
| XX | regions of these amylase genes are used in a new gene expression system. | | | | |
| XX | The system may be used for the expression of heterologous genes in plant | | | | |
| XX | cells and for the large scale production of the encoded products of such | | | | |
| XX | genes. | | | | |
| XX | Nb. some amino acids in this sequence appear to have been wrongly | | | | |
| XX | entered; see feature table and the corresp. DNA file AAO92806, | | | | |
| XX | Sequence 429 AA; | | | | |
| XX | Query Match | | 75.0%; Score 42; | DB 16; | Length 429; |

[illegible]

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVG 9
11:1111
Db 146 NMVNVKVG 153

RESULT 18
ABG69321
ID ABG69321 standard; Protein: 548 AA.

AC ABB49321;

DT 05-FEB-2002 (first entry)

DE Listeria monocytogenes protein #2025.

KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease.

OS Listeria monocytogenes.

PN WO200177335-A2.

PD 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

PA (INSP) INST PASTEUR.

PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Rishi H, Dehoux P,
PI Dussauget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P,
PI Daniels J, Goebel W, Krefit J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L,
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Meduendo E, De Padlos B, Wehlund J, Kaerst U, Entian K, Haut J;
PI Rose M, Voss H;

DR WPI; 2002-010914/01.

PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and
PT related polypeptides -

PS Claim 6; SEQ ID No 2026; 192pp; French.

XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.
XX monocytogenes and related organisms, and for studying genetic
XX polymorphisms and other genomes. The present sequence is a protein
XX encoded by the genome sequence of the present invention. Proteins
XX expressed from the genome sequence are useful for raising specific
XX antibodies, identification of L. monocytogenes and related organisms, and
XX for biosynthesis and biodegradation, especially biosynthesis of Vitamin
XX B12. The genome sequence and proteins encoded by it are also useful for
XX selecting compounds that regulate gene expression and cell replication
XX and modulate L. monocytogenes-related diseases. In addition, the genome
XX sequence and proteins encoded by it are useful in pharmaceutical and
XX vaccines compositions for the treatment or prevention of infections by L.
XX monocytogenes and related organisms.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 548 AA;

Query Match 69.6%; Score 39; DB 23; Length 548;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVG 10
111:111:
Db 137 NMVNVKVG 145

RESULT 19
ABG66859
ID ABG66859 standard; Protein: 54 AA.

AC ABB66859;

DT 24-SEP-2002 (first entry)

DE Human prostate specific protein DEX0283_167.

KW Human; prostate specific protein; cytosolic; PSP; prostate cancer;
KM gene therapy; vaccine; non-cancerous prostatic disease.

OS Homo sapiens.

PN WO200242329-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US45177.

PR 21-NOV-2000; 2000US-252189P.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Macina RA, Recipon H, Sun Y, Liu C;

DR WPI; 2002-500278/53.

PT New prostate specific polypeptides useful for identifying, diagnosing,
PT monitoring, staging, imaging and treating prostate cancer and
PT non-cancerous disease states in prostate -

PS Claim 11; Page 225-226; 248pp; English.

XX The invention relates to an isolated polypeptide that comprises a
XX sequence with 60 % sequence identity to one of 103 prostate specific
XX polypeptide (PSP) sequences (SI), given in specification, or a sequence
XX encoded by a nucleic acid comprising one of 114 prostate specific nucleic
XX acid (PSNA) sequences (S2), given in specification. Also included are
XX a vector comprising the PSNA, a host cell comprising the vector,
XX preparation of the PSP, a polypeptide encoded by the PSNA; an anti-PSP
XX antibody or the antibody or its fragment, a kit for detecting a risk of
XX cancer or presence of cancer in a patient, comprising a unit for
XX determining the presence of the PSP or the PSNA in a sample of a patient
XX and a vaccine comprising the PSP or the PSNA. The PSNA is useful for
XX determining the presence of a prostate specific nucleic acid (PSNA) in a
XX sample. The antibody to the PSP is useful for determining the presence of
XX a prostate specific protein in a sample. The antibody is also useful for
XX treating a patient with prostate cancer, where the administration of the
XX antibody induces an immune response against the prostate cancer cell
XX expressing the nucleic acid molecule or polypeptide. The PSP or the PSNA
XX is useful for diagnosing and monitoring the presence and metastases of
XX prostate cancer in a patient. The PSP is useful as a vaccine component
XX for eliciting a humoral and/or cellular immune response, and for
XX identifying an agonist and antagonist. The PSNA is used in gene therapy,
XX producing transgenic animals and cells, and for producing engineered
XX prostate tissue for treatment and research. The PSNA is useful for
XX detecting prostate cancer by detecting genetic lesions or mutations. The
XX PSP and the PSNA are useful for detecting, diagnosing, monitoring,
XX staging and predicting cancers. The PSP and the PSNA are also useful for
XX identifying prostate tissue, and thus is useful in forensic science,
XX prostate cell differentiation and development and in tissue engineering.
XX The PSP, the PSNA and the antibody are useful for identifying,
XX diagnosing, monitoring, staging, imaging and treating prostate cancer and
XX non-cancerous disease states in prostate tissue. The present
XX sequence is a prostate specific protein (PSP) sequence.

```

XX      Sequence      54 AA:
SQ
Query Match      67.9%; Score 38; DB 23; Length 54;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VMVNVKVG 8
       :| | | | |
Db      43 IMVNVLVG 50

RESULT 20
AAU65532
ID      AAU65532 standard; Protein; 90 AA.
XX
AC      AAU65532;
XX
DT      27-FEB-2002 (first entry)
XX
DE      Propionibacterium acnes immunogenic protein #26428.
XX
KW      SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
KW      uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW      inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW      dermatological; osteopathic; neuroprotectant.
XX
OS      Propionibacterium acnes.
XX
PN      MO200181581-A2.
XX
PD      01-NOV-2001.
XX
PF      20-APR-2001; 2001MO-US12865.
XX
PR      21-APR-2000; 2000US-199047P.
XX      02-JUN-2000; 2000US-208841P.
XX      07-JUL-2000; 2000US-216747P.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI      L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR      WPI: 2001-616774/71.
XX
PT      N-PSDB: AAS59673.
XX
PT      Propionibacterium acnes polypeptides and nucleic acids useful for
PT      vaccinating against and diagnosing infections, especially useful for
PT      treating acne vulgaris -
XX
PS      Example 1; SEQ ID NO 26727; 1069pp; English.
XX
CC      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC      polypeptides. The proteins and their associated DNA sequences are used in
CC      the treatment, prevention and diagnosis of medical conditions caused by
CC      P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC      pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC      P. acnes is also involved in infections of bone, joints and the central
CC      nervous system, however it is particularly involved in the inflammatory
CC      lesions associated with acne vulgaris. A method for detecting the
CC      presence or absence of P. acnes in a patient comprises contacting a
CC      sample with a binding agent that binds to the proteins of the invention
CC      and determining the amount of bound protein in the sample. The
CC      polypeptides may be used as antigens in the production of antibodies
CC      specific for P. acnes proteins. These antibodies can be used to
CC      downregulate expression and activity of P. acnes polypeptides and
CC      therefore treat P. acnes infections. The antibodies may also be used as
CC      diagnostic agents for determining P. acnes presence, for example, by
CC      enzyme linked immunosorbent assay (ELISA).
CC      Note: The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.

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```

XX      Sequence      90 AA:
SQ
Query Match      67.9%; Score 38; DB 22; Length 90;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 NMVNVKVG 9
       :| | | | |
Db      31 NMVNVSIG 38

RESULT 21
ABP74094
ID      ABP74094 standard; Protein; 1077 AA.
XX
AC      ABP74094;
XX
DT      30-JAN-2003 (first entry)
XX
DE      Candida albicans essential protein SEQ ID NO 7931.
XX
KW      Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW      signal transduction; DNA replication; cell division; growth;
KW      proliferation; Candida albicans; fungicide; antifungal.
XX
OS      Candida albicans.
XX
PN      MO200253728-A2.
XX
PD      11-JUL-2002.
XX
PF      26-DEC-2001; 2001MO-US49486.
XX
PR      29-DEC-2000; 2000US-259128P.
XX      20-FEB-2001; 2001US-079202A.
XX      22-AUG-2001; 2001US-314050P.
XX
PA      (ELIT-) ELITRA PHARM INC.
XX
PI      Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX      WPI: 2002-566694/60.
XX      N-PSDB: AB232644.
XX
PT      Constructing strains for identifying gene products as effective targets
PT      for therapeutic intervention, by inactivating in the strain one allele
PT      of a gene and placing other allele of the gene under conditional
PT      expression -
XX
PS      Claim 44; SEQ ID NO 7931; 167pp + Sequence Listing; English.
XX
CC      The invention relates to constructing (M1) a strain of diploid fungal
CC      cells in which both alleles of a gene are modified, comprising modifying
CC      one allele by insertion or replacement by a cassette having an
CC      expressible selectable marker and modifying other allele by a
CC      recombinational, or a promoter replacement fragment with a heterologous
CC      promoter, so that expression of the second allele is regulated by the
CC      promoter. (M1) is useful for constructing a strain of diploid fungal
CC      cells in which both alleles of a gene are modified. The diploid fungal
CC      cells having both alleles modified are useful for identifying a gene that
CC      is essential to the survival or growth of a fungus, a gene that
CC      contributes to the virulence and/or pathogenicity of a fungus, a gene
CC      that contributes to the resistance of a diploid fungus to an antifungal
CC      agent, an antifungal agent that inhibits the growth of a diploid fungus
CC      and for identifying a therapeutic agent for treatment of a mammalian
CC      disease. (M1) is useful for identifying a compound which modulates the
CC      activity of a gene product, preferably enzymatic activity, carbon
CC      compound catabolism, biosynthetic, transporter, transcriptional,
CC      translational, signal transduction, DNA replication and cell division
CC      activity. The method is useful for identifying a compound having the
CC      ability to inhibit growth or proliferation of C. albicans cells and for
CC      treating infection by C. albicans. The present sequence is that of an

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| Query Match | Best Local Similarity | Score | DB | Length |
|----------------|-----------------------|-------|------------|---------|
| Matches | 5; Conservative | 3; | Mismatches | 0; Gaps |
| 1 VNMVNRVGS 10 | 5; Conservative | 3; | Mismatches | 0; Gaps |
| 6 INNVRRGGA 15 | 5; Conservative | 3; | Mismatches | 0; Gaps |

```

XX ABP56006;
XX
XX AC
XX 25-FEB-2003 (first entry)
XX DT
XX Chlamydia psittaci antigen CP4#13 protein SEQ ID NO:31.
XX DE
XX Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
XX KW immunisation; antibacterial; infection.
XX
XX Chlamydia psittaci.
XX OS
XX WO200253588-A2.
XX PN
XX 11-JUL-2002.
XX PD
XX 17-DEC-2001; 2001WO-US48715.
XX PF
XX 15-DEC-2000; 2000US-078269.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;
XX PI WPI: 2002-537942/57.
XX DR N-PSDB; ABQ84762.
XX
XX Vaccine for immunization of animal, preferably bovine, against
XX Chlamydia psittaci, comprises at least one polynucleotide having a C.
XX psittaci sequence, or at least one C. psittaci antigen
XX
XX Claim 5; Page 136; 164pp; English.
XX PS
XX
XX The present invention describes a vaccine (I) for the immunisation of an
XX animal against Chlamydia psittaci comprising at least one polynucleotide
XX (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
XX (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
XX useful for the immunisation of a bovine. The present sequence represents
XX a C. psittaci antigen from the present invention.
XX CC
XX
XX Sequence 232 AA:
XX
XX Query Match 66.1%; Score 37; DB 23; Length 232;
XX Best Local Similarity 75.0%; Pred. No. 2.2e+02;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 3 WVNKVGGS 10
XX 11:11111
XX 180 WVDXAGGS 187
XX
XX DB
XX
XX RESULT 24
XX ABB98215
XX ID ABB98215 standard; Protein; 232 AA.
XX
XX ABB98215;
XX
XX 03-OCT-2002 (first entry)
XX DT
XX Chlamydia polypeptide SEQ ID NO 31.
XX DE
XX Chlamydia; antibacterial; vaccine; immune response; infection.
XX KW Chlamydia; antibacterial; vaccine; immune response; infection.
XX
XX Chlamydia psittaci.
XX OS
XX WO200247718-A2.
XX PN
XX 20-JUN-2002.
XX PD
XX 17-DEC-2001; 2001WO-US48773.
XX PF
XX 15-DEC-2000; 2000US-255839P.
XX PR
XX
XX

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PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PT Johnston SA;
 XX
 DR WPI: 2002-583472/62.
 XX
 DR N-PSDB: ABQ78020.
 XX
 PT Vaccine useful for immunizing an animal, comprising at least one
 PT polynucleotide having a Chlamydia sequence or at least one Chlamydia
 PS antigen -
 XX
 PS Claim 21; Page 144-145; 183pp; English.
 XX
 CC The invention relates to a vaccine (I) comprising at least one
 CC polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at
 CC least one Chlamydia antigen (ABQ8203-ABQ8234) and a pharmaceutically
 CC acceptable carrier. The antigens are useful for immunising an animal, by
 CC providing at least one Chlamydia antigen or its antigenic fragment to the
 CC animal, in an amount effective to induce an immune response in the animal
 CC e.g. mammals including bovine or human. The method is effective to induce
 CC an immune response against C. psittaci, C. pneumoniae or non-Chlamydia
 CC infection. The method further involves administering to the animal an
 CC antigen or an antigenic fragment from Chlamydia species other than
 CC C. psittaci or C. pneumoniae or an antigenic fragment from a
 CC non-Chlamydia species.
 CC
 SO Sequence 232 AA;
 Query Match 66.1%; Score 37; DB 23; Length 232;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 WVNKVGGS 10
 DB 180 WVDKAGGS 187
 11:1111
 RESULT 25
 ABU66271
 ID ABU66271 standard; Protein; 232 AA.
 XX
 AC ABU66271;
 XX
 DT 20-MAY-2003 (first entry)
 XX
 DE C. psittaci protein from genomic DNA sequence CP4 #13.
 XX
 KW Vaccine; chlamydia infection; blindness; mastitis; infertility;
 KW abortion; sexually transmitted disease; atherosclerotic plaque;
 KW community-acquired pneumonia; coronary heart disease; antigen.
 XX
 OS Chlamydia psittaci.
 XX
 PN US2002183272-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 17-DEC-2001; 2001US-0023437.
 XX
 PR 16-AUG-2000; 2000US-225839P.
 XX
 PA (JOHN/) JOHNSTON S A.
 PA (STEM/) STEMEKE-HALE K.
 PA (SYKE/) SYKES K F.
 PA (KALT/) KALTENBOECK B.
 XX
 PI Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
 XX
 DR WPI: 2003-328634/31.
 DR N-PSDB: ABX99187.
 XX
 PT New vaccine comprising a polynucleotide with a Chlamydia sequence or a
 PT Chlamydia antigen, for inducing an immune response against Chlamydia

PT psittaci, Chlamydia pneumoniae, other Chlamydia species, or a
 PT non-Chlamydia infection -
 XX
 PS Claim 21; Page 55; 100pp; English.
 XX
 CC The invention relates to a vaccine comprising a pharmaceutical carrier
 CC and at least one polynucleotide having a Chlamydia sequence or at least
 CC one Chlamydia antigen. The polynucleotide sequences are obtained
 CC from cloned expression library of fragmented genomic DNA (expressed in
 CC the vector PCMV-UbI(+P3). Also included are immunising an animal
 CC comprising providing to the animal at least one Chlamydia antigen or its
 CC antigenic fragment (expressed from the cloned polynucleotides) to induce
 CC an immune response (the proteins are chosen by transforming a vertebrate
 CC animal with constituents of the library and choosing those which elicit
 CC the best immune response, and then expressing those clones in cell
 CC culture and purifying the protein), preparing antibodies against a
 CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
 CC confers immune resistance against chlamydia bacterial infection when
 CC challenged with the Chlamydia species in which the antigen was prepared,
 CC generating an immune response in a vertebrate animal with the identified
 CC antigen, and obtaining antibodies produced in the animal, the antibodies
 CC are used to assay for the presence of chlamydia infection in a vertebrate
 CC animal) and testing for antigens for a first disease state/infectious
 CC agent (comprising determining an antigenic polypeptide or a nucleic acid
 CC encoding an antigenic polypeptide from a second disease state or
 CC infectious agent, obtaining a homologue of the antigenic polypeptide or
 CC a nucleic acid encoding an antigenic polypeptide from a second disease
 CC state or infectious agent for the first disease state/infectious
 CC agent, and testing the homology to see if it is an antigenic
 CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
 CC first disease state or infectious agent). The vaccine, antigens and
 CC polynucleotides are useful for inducing a protective immune response in
 CC vertebrate animals against C. psittaci, C. pneumoniae, other species of
 CC Chlamydia, or a non-Chlamydia infection. The antigens are also useful for
 CC antibody preparation techniques. Chlamydia species are responsible
 CC for blindness, sexually transmitted disease, community-acquired
 CC pneumonia and act as co-factors in atherosclerotic plaque formation in
 CC coronary heart disease. C. psittaci in particular is a cause of mastitis,
 CC infertility and abortion in cattle. The present sequence is one of the
 CC Chlamydia psittaci antigens encoded by a genomic DNA fragment of the
 CC Chlamydia.
 CC
 SO Sequence 232 AA;
 Query Match 66.1%; Score 37; DB 24; Length 232;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 3 WVNKVGGS 10
 DB 180 WVDKAGGS 187
 11:1111
 RESULT 26
 ABB53463
 ID ABB53463 standard; Protein; 527 AA.
 XX
 AC ABB53463;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Lactococcus lactis protein ydgb.
 XX
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
 KW Lactococcus lactis IL1403.
 OS
 XX
 PN FR2807446-A1.
 XX
 PD 12-OCT-2001.
 XX
 PF 11-APR-2000; 2000FR-0004630.
 XX

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PR 11-APR-2000; 2000FR-0004630.
XX
XX (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
XX Bojotline A, Sorokine A, Renault P, Ehrlich SD;
XX
XX WPI: 2002-043418/06.
XX
XX New nucleotide sequence useful in the identification or Lactococcus
XX lactic acid and related species -
XX
XX Claim 6; SEQ ID No 165; 2504pp; French.
XX
XX The present invention is related to a Lactococcus lactis nucleotide
XX sequence (AA050521) and related proteins (AB053300-AB055621). The
XX nucleic acid sequence is useful in the detection and/or amplification of
XX nucleic acid sequence, particularly to identify Lactococcus lactis or
XX related species. The proteins of the invention are useful for the
XX biosynthesis or biodegradation of a composition of interest. The
XX invention helps research in lactic bacteria, particularly useful in the
XX production of yogurt and cheese.
XX Note: The sequence data for this patent is based on equivalent patent
XX WO2001/77334 (published 18-OCT-2001) which is available in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 527 AA;
Query Match 66.1%; Score 37; DB 23; Length 527;
Best Local Similarity 40.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 VNMWKNKXGS 10
DB 127 INMLGNIGCT 136
RESULT 27
AAW88463
ID AAW88463 standard; Protein; 537 AA.
XX
XX AAW88463;
XX
XX 10-MAY-1999 (first entry)
XX
XX Bacillus agaradhaerens xyloglucanase.
XX
XX Xyloglucanase; XEGL; detergent.
XX
XX Bacillus agaradhaerens.
XX
XX WO9902663-A1.
XX
XX 21-JAN-1999.
XX
XX PF 01-JUL-1998; 98WO-DK00290.
XX
XX PR 24-OCT-1997; 97DK-0001213.
XX
XX PR 07-JUL-1997; 97DK-0000822.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bjoernvad ME, Jorgensen PL, Outtrup H, Schuelein M;
XX
XX WPI: 1999-120866/10.
XX
XX N-PSDB; AAX06950.
XX
XX New enzyme preparation comprising a xyloglucanase with an activity
XX of 50 % at pH 7 - useful for improving the properties of cellulosic
XX fibres, yarn, (non)woven fabric, and ratting hemp, jute, flax and
XX linen fibres
XX
XX Claim 18; Page 74-76; 87pp; English.
XX

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CC This polypeptide comprise alkaline xyloglucanase XEGL of
CC Bacillus agaradhaerens NCIMB 40482. The enzyme shows optimal
CC activity at 50 deg C and retains 20% of its activity after 20 min
CC at 60 deg. It retains more than 50% of relative activity in the pH
CC range 5.0-10.5. At pH 7.5, the kcat on xyloglucan was 183/sec and
CC the Km was 0.05 g/l. On CM-cellulose, kcat was 64/sec and Km was
CC 2.2 g/l. An isolated polynucleotide (see AAX06950) can be utilised
CC in the recombinant production of the enzyme. The invention provides
CC expression vectors containing xyloglucanase polynucleotides, and
CC host cells containing these vectors. Xyloglucanase preparations are
CC useful for improving the properties of cellulosic fibres, yarn,
CC (non)woven fabric, and for ratting hemp, jute, flax and linen fibres
CC (claimed). They can also be used in a process for machine treatment
CC of fabrics, and in detergent compositions (claimed). The enzyme
CC preparations exhibit high xyloglucanase activity at alkaline pH
CC without essentially attacking cellulose or cellulose derivatives.
XX
SQ Sequence 537 AA;
Query Match 66.1%; Score 37; DB 20; Length 537;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 VNMWKNKXGS 10
DB 62 VTMQNMOMGS 71
RESULT 28
AAW00383
ID AAW00383 standard; Protein; 574 AA.
XX
XX AAW00383;
XX
XX 31-JAN-1997 (first entry)
XX
XX Bacillus cellulase BCE 113.
XX
XX Cellulase; BCE 113; detergent; surfactant; laundry;
XX tensile strength; antipilling.
XX
XX Bacillus sp. strain CBS 669.93.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX Protein 27..574
XX /label= Sig_peptide
XX /label= Mat.protein
XX /note= "the 63 kDa mature protein is used in
XX detergent compns."
XX
XX MO9634092-A2.
XX
XX 31-OCT-1996.
XX
XX PR 26-APR-1996; 96WO-EP01755.
XX
XX PR 12-MAR-1996; 96US-0614115.
XX
XX PR 28-APR-1995; 95EP-0201115.
XX
XX (GENV ) GENENCOR INT INC.
XX
XX Kotwitz B, Lenting HBW, Maurer K, Van Beckhoven RFMC;
XX
XX Van Solingen P, Weiss A;
XX
XX WPI: 1996-497624/49.
XX
XX Cellulase with low ratio of tensile strength loss to antipilling
XX properties - used in detergent composition which provides
XX anti-greying, softening, anti-wrinkling and colour protection to
XX fabrics
XX

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CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 941 AA;

Query Match

66.1%; Score 37; DB 22; Length 941;

Best Local Similarity 66.7%; Pred. No. 9.5e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10

|||||:

DB 805 NMVVKITGS 813

Search completed: August 29, 2003, 18:44:01
Job time : 32.5714 secs

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ALIGNMENTS

```
RESULT 1
US-09-072-917A-9
; Sequence 9, Application US/09072917A
; Patent No. 6288302
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; APPLICANT: Chan, Ming-Tsair
; TITLE OF INVENTION: Application of Alpha-Amylase Gene
; TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
; Patent No. 6288302
; TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
; TITLE OF INVENTION: Plant Seeds
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072.917A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/509,962
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-072-917A-9
Query Match 82.1%; Score 46; DB 3; Length 435;
Best Local Similarity 88.9%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNMVNVKVG 9
Db 253 VNMVNAVGG 261

RESULT 2
US-07-973-324A-4
; Sequence 4, Application US/07973324A
; Patent No. 5460952
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-4
Query Match 80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNVKVG 10
Db 253 VNMVNAVGA 262

RESULT 3
US-08-343-380-4
; Sequence 4, Application US/08343380
; Patent No. 5712112
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; TITLE OF INVENTION: Gene Expression System Comprising the
; TITLE OF INVENTION: Promoter Region of the Alpha-Amylase Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,380
; FILING DATE: 22-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/973,324
; FILING DATE: 04-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 31149
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-4

Query Match      80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGGA 262

RESULT 4
US-09-072-435-4
Sequence 4, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGGA 262

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGGA 262

RESULT 5
US-09-072-917A-4
Sequence 4, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-4

Query Match      80.4%; Score 45; DB 3; Length 428;
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNMVKNYKGS 10
DB      253 VNMVDRVGGA 262

RESULT 6
US-07-923-692C-6
Sequence 6, Application US/07923692C
Patent No. 5316931
GENERAL INFORMATION:
APPLICANT: Dawson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantlam, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
```

APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,692C
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-692C-6

Query Match 80.4%; Score 45; DB 1; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVKVGGS 10
Db 259 VNMVNVKVGGA 268

RESULT 7
US-08-184-237-6
Sequence 6, Application US/08184237
Patent No. 5589367
GENERAL INFORMATION:
APPLICANT: Donson, Jon

APPLICANT: Dawson, William O.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,237
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 923,692
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-237-6

Query Match 80.4%; Score 45; DB 1; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNVKVGGS 10
Db 259 VNMVNVKVGGA 268

RESULT 8
US-08-482-920-6
Sequence 6, Application US/08482920
Patent No. 5866785
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,920
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 184,237
FILING DATE: 19-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halliuid, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 8129-112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-920-6

Query Match 80.4%; Score 45; DB 2; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;

| | Matches | 7; | Conservative | 3; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|----|---------|-----------|--------------|----|------------|----|--------|----|------|----|
| Qy | 1 | VNMVKNYGS | 10 | | | | | | | |
| Db | 259 | VNMVKNYGS | 268 | | | | | | | |

RESULT 9
US-08-484-341-6
Sequence 6, Application US/08484341
GENERAL INFORMATION:
APPLICANT: Donson, Jon
APPLICANT: Dawson, William O.
APPLICANT: Grantham, George L.
APPLICANT: Turpen, Thomas H.
APPLICANT: Turpen, Ann Myers
APPLICANT: Garger, Stephen J.
APPLICANT: Grill, Laurence K.
TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STATE: CAL
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,341
FILING DATE: 07-JUN-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,237
FILING DATE: <unknown>
APPLICATION NUMBER: US 600,244
FILING DATE: 22-OCT-1990
APPLICATION NUMBER: US 641,617
FILING DATE: 16-JAN-1991
APPLICATION NUMBER: US 310,881
FILING DATE: 17-FEB-1989
APPLICATION NUMBER: US 160,766
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 160,771
FILING DATE: 26-FEB-1988
APPLICATION NUMBER: US 347,637
FILING DATE: 05-MAY-1989
APPLICATION NUMBER: US 363,138
FILING DATE: 08-JUN-1989
APPLICATION NUMBER: US 219,279
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAME: Halliuid, Albert P.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: BIOG-20121 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-484-341-6

Query Match 80.4%; Score 45; DB 3; Length 434;
Best Local Similarity 70.0%; Pred. No. 8.4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 ||||:||||
 Db 259 VNMVDRVGA 268

RESULT 10
 US-08-483-502-6
 ; Sequence 6, Application US/08483502
 ; Patent No. 6284492
 ; GENERAL INFORMATION:
 ; APPLICANT: Donson, Jon
 ; APPLICANT: Dawson, William O.
 ; APPLICANT: Grantham, George L.
 ; APPLICANT: Turpen, Thomas H.
 ; APPLICANT: Turpen, Ann Myers
 ; APPLICANT: Garger, Stephen J.
 ; APPLICANT: Grill, Laurence K.
 ; TITLE OF INVENTION: RECOMBINANT PLANT VIRAL NUCLEIC ACIDS
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
 ; STREET: 1201 New York Avenue N.W., Suite 1000
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,502
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/739,143
 ; FILING DATE:
 ; APPLICATION NUMBER: US 600,244
 ; FILING DATE: 22-OCT-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 641,617
 ; FILING DATE: 16-JAN-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 310,881
 ; FILING DATE: 17-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 160,766
 ; FILING DATE: 26-FEB-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 160,771
 ; FILING DATE: 26-FEB-1988
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 347,637
 ; FILING DATE: 05-MAY-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 363,138
 ; FILING DATE: 08-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 219,279
 ; FILING DATE: 15-JUL-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ihnen, Jeffrey L.
 ; REGISTRATION NUMBER: 28,957
 ; REFERENCE/DOCKET NUMBER: 18604-090574
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-962-4810
 ; TELEFAX: 202-962-8300
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 434 amino acids
 ; TYPE: amino acid

; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-502-6

Query Match 80.4%; Score 45; DB 3; Length 434;
 Best Local Similarity 70.0%; Pred. No. 8.4;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 ||||:||||
 Db 259 VNMVDRVGA 268

RESULT 11
 US-09-726-651A-6
 ; Sequence 6, Application US/09726651A
 ; Patent No. 6448046
 ; GENERAL INFORMATION:
 ; APPLICANT: Donson, Jon
 ; APPLICANT: Dawson, William O.
 ; APPLICANT: Grantham, George L.
 ; APPLICANT: Turpen, Thomas H.
 ; APPLICANT: Turpen, Ann M.
 ; APPLICANT: Garger, Stephen J.
 ; APPLICANT: Grill, Laurence K.
 ; TITLE OF INVENTION: RECOMBINANT ANIMAL VIRUS NUCLEIC ACIDS
 ; FILE REFERENCE: 008010023CNU501
 ; CURRENT APPLICATION NUMBER: US/09/726,651A
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: 08/483,502
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/184,237
 ; PRIOR FILING DATE: 1994-01-19
 ; PRIOR APPLICATION NUMBER: 07/923,692
 ; PRIOR FILING DATE: 1992-07-31
 ; PRIOR APPLICATION NUMBER: 07/600,244
 ; PRIOR FILING DATE: 1990-10-22
 ; PRIOR APPLICATION NUMBER: 07/641,617
 ; PRIOR FILING DATE: 1991-01-16
 ; PRIOR APPLICATION NUMBER: 07/737,899
 ; PRIOR FILING DATE: 1991-07-26
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 434
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: CLONE: alpha-amylase
 ; OTHER INFORMATION: protein
 ; US-09-726-651A-6

Query Match 80.4%; Score 45; DB 4; Length 434;
 Best Local Similarity 70.0%; Pred. No. 8.4;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGS 10
 ||||:||||
 Db 259 VNMVDRVGA 268

RESULT 12
 US-09-510-322A-8
 ; Sequence 8, Application US/09510322A
 ; Patent No. 6391557
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox Chase Cancer Center
 ; TITLE OF INVENTION: Nucleic Acid Encoding a Mismatch
 ; FILE REFERENCE: 9503dna
 ; CURRENT APPLICATION NUMBER: US/09/510,322A
 ; CURRENT FILING DATE: 2000-02-22
 ; NUMBER OF SEQ ID NOS: 11


```

: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 8
: LENGTH: 267
: TYPE: prt
: ORGANISM: Plant
US-09-510-322A-8

```

| | | | | |
|-----------------------|--------|---------------|-------|---------------------------------|
| Query Match | 67.9%; | Score 38; | DB 4; | Length 267; |
| Best Local Similarity | 55.6%; | Pred. NO. 69; | | |
| Matches | 5; | Conservative | 3; | Mismatches 1; Indels 0; Gaps 0; |

```
QY      2 NTWVKVGG 10
      ||::||
Db     255 NTWINEIHGS 263
```

RESULT 13
 US-09-252-991A-24308
 Sequence 24308, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-16
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 3142
 SEQ ID NO 24308
 LENGTH: 460
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-24308

```

Query Match      66.1%; Score 37; DB 4; Length 460;
Best local Similarity 60.0%; Pred. No. 1,7e-02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 VNNVNNKVGGS 10
        | : : |||||
Db      407 VTWLETVGGS 416

```

```

1  RESULT 14
2  US-09-110-959A-4
3  Sequence 4, Application US/09110959A
4  Patent No. 6268197
5  GENERAL INFORMATION:
6  APPLICANT: Schultein, Martin
7  APPLICANT: Outtrup, Heile
8  APPLICANT: Jorgensen, Per Lina
9  APPLICANT: Bjornvad, Basse Eskelund
10 TITLE OF INVENTION: Alkaline Xyloglucanase
11 FILE REFERENCE: 5206 200-US
12 CURRENT APPLICATION NUMBER: US/09/110,959A
13 CURRENT FILING DATE: 1998-07-07
14 PRIOR APPLICATION NUMBER: 08822/97
15 PRIOR FILING DATE: 1997-07-07
16 PRIOR APPLICATION NUMBER: 1213/97
17 PRIOR FILING DATE: 1997-10-24
18 PRIOR APPLICATION NUMBER: 60/054,039
19 PRIOR FILING DATE: 1997-07-28
20 PRIOR APPLICATION NUMBER: 60/063,694
21 PRIOR FILING DATE: 1997-10-28
22 NUMBER OF SEQ ID NOS: 14
23 SOFTWARE: FASTSD for Windows Version 4.0
24 SEQ ID NO: 4
25 LENGTH: 537
26 TYPE: prt

```

ORGANISM: *Bacillus agaradhaerens* NCIMB 40482
US-09-110-959A-4

| | | | | |
|-----------------------|--------|------------------|-------|---------------------------------|
| Query Match | 66.1%; | Score 37; | DB 3; | Length 537; |
| Best Local Similarity | 60.0%; | Pred. No. 2e+02; | | |
| Matches | 6; | Conservative | 2; | Mismatches 2; Indels 0; Gaps 0; |

| | | | |
|----|----|------------|----|
| Qy | 1 | VNVVNKVGGS | 10 |
| | | : | |
| Db | 62 | VTVQNQMGGS | 71 |

```

1      RESULT 15
2      US-09-107-532A-4136
3      : Sequence 4136, Application US/09107532A
4      : Patent No. 6583275
5      :
6      GENERAL INFORMATION:
7      APPLICANT: Lynn A Doucette-Stamm and David Bush
8      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
9      ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
10     :
11     NUMBER OF SEQUENCES: 7310
12     CORRESPONDENCE ADDRESS:
13     ADDRESS: GENOME THERAPEUTICS CORPORATION
14     STREET: 100 Beaver Street
15     CITY: Waltham
16     STATE: Massachusetts
17     COUNTRY: USA
18     ZIP: 02354
19
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: CD-ROM ISO9660
22     COMPUTER: PC
23     OPERATING SYSTEM: <unknown>
24     SOFTWARE: ASCII
25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/09/107,532A
28     FILING DATE: 30-Jun-1998
29
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: 60/085,598
32     FILING DATE: 14 May 1998
33     APPLICATION NUMBER: 60/051571
34     FILING DATE: July 2, 1997
35
36     ATTORNEY/AGENT INFORMATION:
37     NAME: Arinietello, Pamela Deneke
38     REGISTRATION NUMBER: 40,489
39     REFERENCE/DOCKET NUMBER: GTC-012
40
41     TELECOMMUNICATION INFORMATION:
42     TELEPHONE: (781)893-8277
43     TELEFAX: (781)893-8277
44
45     INFORMATION FOR SEQ ID NO: 4136:
46     SEQUENCE CHARACTERISTICS:
47     LENGTH: 544 amino acids
48     TYPE: amino acid
49     TOPOLOGY: linear
50     MOLECULE TYPE: protein
51     HYPOTHETICAL: YES
52     ORIGINAL SOURCE:
53     ORGANISM: Enterococcus faecium
54     FEATURE:
55     NAME/KEY: misc_feature
56     LOCATION: (B) LOCATION 1..544
57     SEQUENCE DESCRIPTION: SEQ ID NO: 4136:
58
59     US-09-107-532A-4136

```

| | | | | |
|-----------------------|--------|------------------|-------|---------------|
| Query Match | 66.1%; | Score 37; | DB 4; | Length 544; |
| Best Local Similarity | 66.7%; | Pred. No. 2e+02; | | |
| Matches | 6; | Conservative | 2; | Mismatches 1; |
| | | | | Indels 0; |
| | | | | Gaps 0; |
| Qy | 2 | MMYMKVGGGS | 10 | |
| | : | !!!:!!! | | |
| Db | 132 | DWMSKEGGGS | 140 | |

RESULT 16

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5530:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (8) LOCATION 1...427
SEQUENCE DESCRIPTION: SEQ ID NO: 5530:
US-09-107-532A-5530

Query Match 64.3%; Score 36; DB 1; Length 427;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 10
DB 75 INWVLGVGR 84

RESULT 19
US-07-973-324A-2
Sequence 2, Application US/07973324A
Patent No. 5460952
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region Of The Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,324A
FILING DATE: 04-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-973-324A-2

Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9

DB 255 VNMNAQAVGG 263

RESULT 20
US-08-343-380-2
Sequence 2, Application US/08343380
Patent No. 5712112
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
TITLE OF INVENTION: Gene Expression System Comprising the
TITLE OF INVENTION: Promoter Region Of The Alpha-Amylase Genes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,380
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 31149
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-380-2

Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9
DB 255 VNMNAQAVGG 263

RESULT 21
US-09-072-435-2
Sequence 2, Application US/09072435
Patent No. 6215051
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: GENE EXPRESSION SYSTEM COMPRISING THE
TITLE OF INVENTION: PROMOTER REGION OF THE ALPHA-AMYLASE GENES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago

STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,792
FILING DATE: 29-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/973,324
FILING DATE: 04-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-435-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 3; Length 438;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9
DB 255 VNMQAQAVG 263

RESULT 22
US-09-072-917A-2
Sequence 2, Application US/09072917A
Patent No. 6288302
GENERAL INFORMATION:
APPLICANT: Yu, Su-May
APPLICANT: Liu, Li-Fei
APPLICANT: Chan, Ming-Tsair
TITLE OF INVENTION: Application of Alpha-Amylase Gene
TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
Patent No. 6288302
TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
TITLE OF INVENTION: Plant Seeds
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072.917A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/509,962
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28123/34257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-072-917A-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 3; Length 438;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 9
DB 255 VNMQAQAVG 263

RESULT 23
US-09-527-236A-26
Sequence 26, Application US/09527236A
Patent No. 6358508
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375Pl
CURRENT APPLICATION NUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/052,991
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 09/095,094
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/126,019
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/134,220
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-527-236A-26

Query Match
Best Local Similarity 62.5%; Score 35; DB 4; Length 67;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNMVNRKVG 8
DB 35 IKMVKNTG 42

RESULT 24
US-08-983-607-47
Sequence 47, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-67

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNVGGG 10
DB 110 VNMOTKSGGT 119

RESULT 27
US-09-056-556-66
Sequence 66, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-66

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNVGGG 10
DB 110 VNMOTKSGGT 119

RESULT 28

US-09-072-596-67
Sequence 67, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-67

Query Match 62.5%; Score 35; DB 4; Length 132;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNVGGG 10
DB 110 VNMOTKSGGT 119

RESULT 29
US-09-333-593A-4
Sequence 4, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 303
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-4

Query Match 62.5%; Score 35; DB 4; Length 303;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNMVKNYVG 8
: |||| |
Db 250 IKVWKTG 257

RESULT 30
US-08-818-112-79
Sequence 79, Application us/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vardick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411c6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-79

Query Match 62.5%; Score 35; DB 3; Length 355;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 VNMVKNYVGS 10
||| | ||:

Db 333 VNMQTSKGT 342

Search completed: August 29, 2003, 18:44:41
Job time: 11.5714 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:42:11 ; Search time 15.7143 Seconds
(without alignments)
87.043 Million cell updates/sec

Title: US-09-830-876-3
Perfect score: 56
Sequence: 1 VNMVNRVGS 10

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues
Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 45 | 80.4 | 434 | 12 | US-10-280-679B-6 |
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| 3 | 38 | 67.9 | 147 | 15 | US-10-156-761-13047 |
| 4 | 37 | 66.1 | 153 | 15 | US-10-156-761-7874 |
| 5 | 37 | 66.1 | 222 | 14 | US-10-023-437-31 |
| 6 | 37 | 66.1 | 222 | 14 | US-10-023-437-31 |
| 7 | 37 | 66.1 | 222 | 14 | US-10-023-437-31 |
| 8 | 37 | 66.1 | 222 | 14 | US-10-023-437-31 |
| 9 | 36 | 64.3 | 149 | 16 | US-10-080-170-434 |
| 10 | 36 | 64.3 | 439 | 12 | US-10-228-063-51 |
| 11 | 36 | 64.3 | 519 | 15 | US-10-081-872-212 |
| 12 | 36 | 64.3 | 550 | 9 | US-09-967-477B-2 |
| 13 | 36 | 64.3 | 925 | 10 | US-09-815-242-13987 |
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| 16 | 35 | 62.5 | 67 | 14 | US-10-041-574-26 | Sequence 26, App1 |
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| 18 | 35 | 62.5 | 132 | 9 | US-09-759-143-848 | Sequence 848, App |
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| 20 | 35 | 62.5 | 132 | 9 | US-09-780-663-848 | Sequence 848, App |
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| 22 | 35 | 62.5 | 132 | 9 | US-09-822-827-848 | Sequence 848, App |
| 23 | 35 | 62.5 | 132 | 10 | US-09-895-793-819 | Sequence 819, App |
| 24 | 35 | 62.5 | 132 | 10 | US-09-895-793-848 | Sequence 848, App |
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| 26 | 35 | 62.5 | 132 | 10 | US-09-895-814-848 | Sequence 848, App |
| 27 | 35 | 62.5 | 132 | 12 | US-10-084-843-66 | Sequence 66, App1 |
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| 29 | 35 | 62.5 | 132 | 12 | US-10-144-678A-819 | Sequence 819, App |
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| 35 | 35 | 62.5 | 303 | 8 | US-08-916-625B-4 | Sequence 4, App11 |
| 36 | 35 | 62.5 | 318 | 10 | US-09-738-626-4710 | Sequence 4710, Ap |
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| 39 | 35 | 62.5 | 367 | 10 | US-09-801-368-318 | Sequence 318, App |
| 40 | 35 | 62.5 | 411 | 8 | US-08-916-625B-2 | Sequence 2, App11 |
| 41 | 35 | 62.5 | 411 | 9 | US-09-828-739-2 | Sequence 2, App11 |
| 42 | 35 | 62.5 | 411 | 9 | US-09-757-421-4 | Sequence 4, App11 |
| 43 | 35 | 62.5 | 411 | 9 | US-09-874-138-2 | Sequence 2, App11 |
| 44 | 35 | 62.5 | 411 | 10 | US-09-887-879-11 | Sequence 11, App1 |
| 45 | 35 | 62.5 | 411 | 10 | US-09-811-088-6 | Sequence 6, App1 |
| 46 | 35 | 62.5 | 411 | 10 | US-09-993-964-11 | Sequence 11, App1 |
| 47 | 35 | 62.5 | 411 | 12 | US-10-247-383-11 | Sequence 11, App1 |
| 48 | 35 | 62.5 | 411 | 12 | US-10-288-937-1 | Sequence 1, App11 |
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| 54 | 35 | 62.5 | 411 | 14 | US-10-207-655-194 | Sequence 194, App |
| 55 | 35 | 62.5 | 411 | 15 | US-10-314-410-6 | Sequence 6, App1 |
| 56 | 35 | 62.5 | 432 | 15 | US-10-081-816-11 | Sequence 11, App1 |
| 57 | 35 | 62.5 | 436 | 15 | US-10-081-816-11 | Sequence 11, App1 |
| 58 | 35 | 62.5 | 439 | 15 | US-10-156-761-1438 | Sequence 1438, A |
| 59 | 35 | 62.5 | 440 | 9 | US-09-757-421-2 | Sequence 2, App11 |
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| 62 | 35 | 62.5 | 445 | 15 | US-10-156-761-14137 | Sequence 14137, A |
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| 70 | 33 | 58.9 | 67 | 10 | US-10-041-574-25 | Sequence 25, App1 |
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| 73 | 33 | 58.9 | 98 | 9 | US-09-905-243-51 | Sequence 51, App |
| 74 | 33 | 58.9 | 210 | 16 | US-10-080-170-439 | Sequence 439, App |
| 75 | 33 | 58.9 | 211 | 10 | US-09-728-626-1433 | Sequence 1433, App |
| 76 | 33 | 58.9 | 310 | 11 | US-10-141-321A-36 | Sequence 36, App1 |
| 77 | 33 | 58.9 | 316 | 15 | US-10-141-321A-36 | Sequence 36, App1 |
| 78 | 33 | 58.9 | 316 | 15 | US-10-141-321A-36 | Sequence 36, App1 |
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89 33 58.9 468 15 US-10-226-318-2 Sequence 2, Appl1
90 33 58.9 468 15 US-10-175-902-2 Sequence 2, Appl1
91 33 58.9 477 15 US-10-060-036-164 Sequence 164, Appl
92 33 58.9 490 14 US-10-016-634A-175 Sequence 175, App
93 33 58.9 503 15 US-10-156-761-8095 Sequence 8095, Ap
94 33 58.9 597 9 US-09-815-242-13226 Sequence 13226, A
95 33 58.9 695 9 US-09-945-258-18 Sequence 18, Appl1
96 33 58.9 747 11 US-09-824-574-6 Sequence 6, Appl1
97 33 58.9 965 11 US-09-842-484A-2 Sequence 4, Appl1
98 33 58.9 965 11 US-09-842-484A-4 Sequence 2, Appl1
99 33 58.9 965 15 US-10-184-485-3 Sequence 3, Appl1
100 33 58.9 965 15 US-10-217-613-3 Sequence 3, Appl1
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ALIGNMENTS

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RESULT 1
; Sequence 6, Application US/10280679B
; Publication No. US20030150019A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
; FILE REFERENCE: LSBC-0109-US03
; CURRENT APPLICATION NUMBER: US/10/280,679B
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 09/557,941
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 08/484,341
; PRIOR FILING DATE: 1995-06-07/923,692
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; PRIOR APPLICATION NUMBER: 07/600,244
; PRIOR FILING DATE: 1990-10-22
; PRIOR APPLICATION NUMBER: 07/641,617
; PRIOR FILING DATE: 1991-01-16
; PRIOR APPLICATION NUMBER: 07/737,899
; PRIOR FILING DATE: 1991-07-26
; PRIOR APPLICATION NUMBER: 07/739,143
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/310,881
; PRIOR FILING DATE: 1989-02-17
; PRIOR APPLICATION NUMBER: 07/160,766
; PRIOR FILING DATE: 1988-02-26
; PRIOR APPLICATION NUMBER: 07/160,771
; PRIOR FILING DATE: 1988-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Rice alpha-amylase
US-10-280-679B-6

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DB 259 VNWVNRKVG 268
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RESULT 2

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US-10-001-870-167
; Sequence 167, Application US/10001870
; Publication No. US20020150924A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
```

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; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
; FILE REFERENCE: DEX-0283
; CURRENT APPLICATION NUMBER: US/10/001,870
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,189
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-870-167

Query Match      67.9%; Score 38; DB 14; Length 54;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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DB 43 VNWVNRKVG 50
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RESULT 3
US-10-156-761-13047
; Sequence 13047, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
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; LENGTH: 147
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13047
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Best Local Similarity 71.4%; Pred. No. 50;
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DB 47 VNWVNRKVG 53
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RESULT 4

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US-10-156-761-7974
; Sequence 7974, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRO
```

FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7974
LENGTH: 153
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-7974

Query Match 66.1%; Score 37; DB 15; Length 153;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 MNVNRVGG 9
DB 50 HWYRVGG 57

RESULT 5
US-10-023-437-31
Sequence 31, Application US/10023437
Publication No. US20020183272A1
GENERAL INFORMATION:
APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEWART-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
FILE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
FILE REFERENCE: US/10/023,437
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 232
TYPE: PRT
ORGANISM: Chlamydia psittaci
US-10-023-437-31

Query Match 66.1%; Score 37; DB 14; Length 232;
Best Local Similarity 75.0%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WYNKYGS 10
DB 180 WYDKAGS 187

RESULT 6
US-09-863-547B-2
Sequence 2, Application US/09863547B
Patent No. US2002012816A1
GENERAL INFORMATION:
APPLICANT: Henkel G&A
APPLICANT: Hermann, Lentus B. M.
APPLICANT: Van Beckhoven, Rudolf F. W. C.
APPLICANT: Maurer, Karl-Heinz
APPLICANT: Kottwitz, Beatrix
APPLICANT: Weiss, Albrecht
APPLICANT: Van Solingen, Pieter
TITLE OF INVENTION: Detergents Comprising Cellulases
FILE REFERENCE: H 1920 A
CURRENT APPLICATION NUMBER: US/09/863,547B
CURRENT FILING DATE: 2002-02-13

PRIOR APPLICATION NUMBER: US 08/945,574
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: PCT/EP96/01755
PRIOR FILING DATE: 1996-04-26
PRIOR APPLICATION NUMBER: US 08/614,115
PRIOR FILING DATE: 1996-03-12
PRIOR APPLICATION NUMBER: EP 95201115.3
PRIOR FILING DATE: 1995-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 574
TYPE: PRT
ORGANISM: Bacillus sp. 669.93
US-09-863-547B-2

Query Match 66.1%; Score 37; DB 10; Length 574;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 WYNKYGS 10
DB 87 WYENRIGGA 96

RESULT 7
US-10-023-437-33
Sequence 33, Application US/10023437
Publication No. US20020183272A1
GENERAL INFORMATION:
APPLICANT: JOHNSTON, STEPHEN A.
APPLICANT: STEWART-HALE, KATHERINE
APPLICANT: SYKES, KATHRYN F.
APPLICANT: KALTENBOECK, BERNHARD
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC AC
FILE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
FILE REFERENCE: US/10/023,437
CURRENT APPLICATION NUMBER: US/10/023,437
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/225,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 969
TYPE: PRT
ORGANISM: Chlamydia psittaci
US-10-023-437-33

Query Match 66.1%; Score 37; DB 14; Length 969;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WYNKYGS 10
DB 374 WYDKAGS 381

RESULT 8
US-10-080-170-434
Sequence 434, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495,0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 434
; LENGTH: 149
; TYPE: PRF
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-434

Query Match
Best Local Similarity 64.3%; Score 36; DB 16; Length 149;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVNKVGGS 10
DB 36 WVNAGCT 43

RESULT 9
US-10-228-063-51
; Sequence 51, Application US/10228063
; Publication No. US20030135865A1
; GENERAL INFORMATION:
; APPLICANT: Lanhuan, Mike
; TITLE OF INVENTION: Self-processing plants and plant parts
; FILE REFERENCE: 109846.317
; CURRENT APPLICATION NUMBER: US/10/228,063
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 439
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-228-063-51

Query Match
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Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 257 VNNQAAGG 265

RESULT 10
US-10-081-872-212
; Sequence 212, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kervu, Janne S.
; APPLICANT: Slupka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-108001
; CURRENT APPLICATION NUMBER: US/10/081,872
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 496
```

```
; TYPE: PRF
; ORGANISM: Environmental
US-10-081-872-212

Query Match
Best Local Similarity 64.3%; Score 36; DB 15; Length 496;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VNVNKKYGG 10
DB 321 VDMVDATGGS 330

RESULT 11
US-09-967-477B-2
; Sequence 2, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haijing Hong
; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
; FILE REFERENCE: BM2-001
; CURRENT APPLICATION NUMBER: US/09/967,477B
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 519
; TYPE: PRF
; ORGANISM: Thraustochytrium sp.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 462
; OTHER INFORMATION: Xaa = Gly
US-09-967-477B-2

Query Match
Best Local Similarity 64.3%; Score 36; DB 10; Length 519;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WVNKVGGS 9
DB 194 WVNKVG 200

RESULT 12
US-09-815-242-13987
; Sequence 13987, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes In
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
```

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 13987
;; LENGTH: 550
;; TYPE: PRT
;; ORGANISM: *Salmonella typhi*
;; FEATURE:
;; NAME/KEY: VARIANT
;; LOCATION: (1)...(550)
;; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-13987

Query Match 64.3%; Score 36; DB 9; Length 550;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMVNRVGS 10
11:1111
DB 139 NMOSKFGS 147

RESULT 13
US-09-924-097-14
;; Sequence 14, Application US/09924097
;; Patent No. US20020156240A1
;; GENERAL INFORMATION:
;; APPLICANT: TOMONO, Jun
;; APPLICANT: NOMURA, Toshiiko
;; APPLICANT: SAGAWA, Hiroaki
;; APPLICANT: KATO, Ikunoshin
;; TITLE OF INVENTION: ALPHA-AGARASE AND PROCESS FOR PRODUCING THE SAME
;; FILE REFERENCE: TOMONO-1
;; CURRENT APPLICATION NUMBER: US/09/924,097
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: JP00/00966
;; PRIOR FILING DATE: 2000-02-21
;; PRIOR APPLICATION NUMBER: 11-44890
;; PRIOR FILING DATE: 1999-02-23
;; PRIOR APPLICATION NUMBER: 11-198852
;; PRIOR FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 14
;; LENGTH: 925
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Amino acid sequence of agarase 1-7
US-09-924-097-14

Query Match 64.3%; Score 36; DB 10; Length 925;
Best Local Similarity 75.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNRVGS 9
1111:11
DB 378 NMVNOVGS 385

RESULT 14
US-10-156-761-9313
;; Sequence 9313, Application US/10156761
;; Publication No. US20030119018A1

;; GENERAL INFORMATION:
;; APPLICANT: OMURA, SATOSHI
;; APPLICANT: IKEDA, HARUO
;; APPLICANT: ISHIKAWA, JUN
;; APPLICANT: HORIKAWA, HIROSHI
;; APPLICANT: SHIBA, TADAYOSHI
;; APPLICANT: SAKAKI, YOSHIYUKI
;; APPLICANT: HATTORI, MASAHIRA
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 248-262
;; CURRENT APPLICATION NUMBER: US/10/156,761
;; PRIOR FILING DATE: 2002-05-23
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO: 9313
;; LENGTH: 964
;; TYPE: PRT
;; ORGANISM: *Streptomyces avermitilis*
US-10-156-761-9313

Query Match 64.3%; Score 36; DB 15; Length 964;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMVNRVGS 8
11:1111
DB 684 NMINKLG 690

RESULT 15
US-09-756-854-26
;; Sequence 26, Application US/09756854
;; Patent No. US20020164684A1
;; GENERAL INFORMATION:
;; APPLICANT: NI, Jian
;; Yu, Guo-Liang
;; Fan, Ping
;; Gentz, Reiner
;; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR8
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: MD
;; COUNTRY: US
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/756,854
;; FILING DATE: 10-Jan-2001
;; CLASSIFICATION: <unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/095,094
;; FILING DATE: <unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hoover, Kenley K.
;; REGISTRATION NUMBER: 40,302
;; REFERENCE/DOCKET NUMBER: PF375
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-309-8439
;; TELEFAX: 301-309-8504
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 67 amino acids
;; type: amino acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-756-854-26

Query Match      62.5%; Score 35; DB 10; Length 67;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 VNMVNKVG 8
       : |||||
Db      35 IKWVNKTG 42

RESULT 16
US-10-041-574-26
; Sequence 26, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-26

Query Match      62.5%; Score 35; DB 14; Length 67;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1 VNMVNKVG 8
       : |||||
Db      35 IKWVNKTG 42

RESULT 17
US-09-759-143-819
; Sequence 819, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
```

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; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-759-143-819

Query Match      62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 VNMVNKVGGS 10
       : ||| | ||:
Db      110 VNMOTKSGGT 119

RESULT 18
US-09-759-143-848
; Sequence 848, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 848
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-848

Query Match      62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      1 VNMVNKVGGS 10
       : ||| | ||:
Db      110 VNMOTKSGGT 119

RESULT 19
US-09-780-669-819
; Sequence 819, Application US/09780669
```

```
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-819

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 20
US-09-780-669-848
Sequence 848, Application US/09780669
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
```

```
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-848

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 21
US-09-822-827-819
Sequence 819, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-819

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNKVGGS 10
DB 110 VNMOTKSGGT 119

RESULT 22
US-09-822-827-848
Sequence 848, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-848

Query Match          62.5%; Score 35; DB 9; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNKVGGS 10
DB 110 VNMOTKSGGT 119
```

```

RESULT 23
US-09-895-793-819
; Sequence 819, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-895-793-819

Query Match          62.5%; Score 35; DB 10; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 VNMVNRKVGGS 10
      ||| | ||:
Db      110 VNMOTKSGGT 119

RESULT 24
US-09-895-793-848
; Sequence 848, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

```

```

; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 848
; LENGTH: 132
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-895-793-848

Query Match          62.5%; Score 35; DB 10; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 VNMVNRKVGGS 10
      ||| | ||:
Db      110 VNMOTKSGGT 119

RESULT 25
US-09-895-814-819
; Sequence 819, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 819
; LENGTH: 132
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-895-814-819

Query Match          62.5%; Score 35; DB 10; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 VNMVNRKVGGS 10
      ||| | ||:
Db      110 VNMOTKSGGT 119

```


RESULT 26
US-09-895-814-848
Sequence 848, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-814-848

Query Match 62.5% Score 35; DB 10; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNVGGG 10
DB 110 VNMVKNVGGT 119

RESULT 27
US-10-084-843-66
Sequence 66, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-084-843-66

Query Match 62.5% Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVKNVGGG 10
DB 110 VNMVKNVGGT 119

RESULT 28
US-10-193-002-67
Sequence 67, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, David C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-193-002-67

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMVTKSGGT 119

RESULT 29
US-10-144-678A-819
Sequence 819, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ya
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 819
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-819

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMVTKSGGT 119

RESULT 30
US-10-144-678A-848
Sequence 848, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William T.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ya
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 848
LENGTH: 132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-848

Query Match 62.5%; Score 35; DB 12; Length 132;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVNVGGS 10
111 111:
DB 110 VNMVTKSGGT 119

Search completed: August 29, 2003, 18:47:49
Job time: 17.7143 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:44:06 ; Search time 10.2857 Seconds
(without alignments)
93.497 Million cell updates/sec

Title: US-09-830-876-3
Perfect score: 56
Sequence: 1 VNMVNRVGGG 10

Scoring table: BIOSUM62
Gap 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 56 | 100.0 | 429 | 1 JE0406 | alpha-amy-lase (EC |
| 2 | 49 | 87.5 | 383 | 1 ALR20C | alpha-amy-lase (EC |
| 3 | 48 | 85.7 | 438 | 1 ALBH | alpha-amy-lase (EC |
| 4 | 47 | 83.9 | 427 | 1 ALBHB | alpha-amy-lase (EC |
| 5 | 47 | 83.9 | 437 | 2 S07040 | alpha-amy-lase (EC |
| 6 | 46 | 82.1 | 435 | 2 S12625 | alpha-amy-lase (EC |
| 7 | 45 | 80.4 | 428 | 2 JC7137 | alpha-amy-lase (EC |
| 8 | 45 | 80.4 | 434 | 2 S10013 | alpha-amy-lase (EC |
| 9 | 45 | 80.4 | 440 | 2 S12775 | alpha-amy-lase (EC |
| 10 | 42 | 75.0 | 440 | 2 S14958 | alpha-amy-lase (EC |
| 11 | 42 | 75.0 | 680 | 2 H64206 | fructose-permease |
| 12 | 41 | 73.2 | 689 | 2 S69535 | hypothetical prote |
| 13 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 14 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 15 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 16 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 17 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 18 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 19 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 20 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 21 | 40 | 71.4 | 340 | 2 T28856 | hypothetical prote |
| 22 | 39 | 69.6 | 157 | 2 AC1312 | thioredoxin homolo |
| 23 | 39 | 69.6 | 157 | 2 AC1312 | thioredoxin homolo |
| 24 | 39 | 69.6 | 157 | 2 AC1312 | thioredoxin homolo |
| 25 | 39 | 69.6 | 157 | 2 AC1312 | thioredoxin homolo |
| 26 | 38 | 67.9 | 270 | 2 S17828 | alpha, alpha-phosph |
| 27 | 38 | 67.9 | 270 | 2 S17828 | alpha, alpha-phosph |
| 28 | 38 | 67.9 | 270 | 2 S17828 | alpha, alpha-phosph |
| 29 | 38 | 67.9 | 270 | 2 S17828 | alpha, alpha-phosph |

| | | | | | |
|-----|----|------|------|----------|--------------------|
| 30 | 38 | 67.9 | 627 | 2 AD2161 | alkaline phosphata |
| 31 | 37 | 66.1 | 1078 | 2 S48842 | DNA-directed RNA p |
| 32 | 37 | 66.1 | 132 | 2 G69272 | conserved hypothec |
| 33 | 37 | 66.1 | 1228 | 1 A69094 | delta 1 pyroline |
| 34 | 37 | 66.1 | 278 | 2 T49276 | hypothetical prote |
| 35 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 36 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 37 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 38 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 39 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 40 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 41 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 42 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 43 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 44 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 45 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 46 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
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| 52 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 53 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 54 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 55 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
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| 59 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
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| 75 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 76 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 77 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 78 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 79 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 80 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 81 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 82 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 83 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 84 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 85 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 86 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 87 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 88 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
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| 90 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 91 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 92 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
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| 94 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 95 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 96 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 97 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 98 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 99 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |
| 100 | 37 | 66.1 | 417 | 2 S09333 | DNA-directed RNA p |

alkaline phosphata
DNA-directed RNA p
conserved hypothec
delta 1 pyroline
hypothetical prote
DNA-directed RNA p
probable MFS trans
hypothetical prote
endo-beta-1,4-gluc
ent-kaurene syntha
DNA-directed RNA p
hypothetical prote
hypothetical prote
probable S-adenosyl
3-ketoacyl-CoA thi
hypothetical prote
uracil permease ur
alpha-amy-lase (EC
alpha-amy-lase (EC
alpha-amy-lase (EC
hypothetical prote
alpha, alpha-phosph
alpha, alpha-phosph
alpha, alpha-phosph
trehalase-6-phosph
hypothetical prote
MDH flavin oxidor
MDH flavin oxidor
probable protein t
DNA-directed RNA p
spectrin alpha cha
L-plastin - rabbit
hypothetical prote
hypothetical prote
probable phosphor
2-keto-3-deoxygluc
hypothetical prote
SS081 protein - ye
precocorrin-6y-depen
alpha-amy-lase (EC
hypothetical prote
major facilitator
cellulase (EC 3.2.
cellulase (EC 3.2.
NADH2 dehydrogenas
probable WD-domain
alpha, alpha-phosph
trehalase 6-P hydr
T-plastin - human
T-plastin - rat (f
65k macrophage pro
plastin, interstina
T-plastin - human
fibrin - chicken
ferric-pseudocacti
hypothetical prote
preproctein transio
telomerase reverse
callose synthase c
toxin-like outer m
toxin-like outer m
Ig heavy chain V r
Ig heavy chain V-I
probable ribosome-
Ig heavy chain var

ALIGNMENTS

```

RESULT 1
JE0406
alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Hordeum vulgare (barley)
C>Date: 17-Apr-1993 #sequence_revision 21-Jan-1997 #text_change 18-Jun-1999
C:Accession: JE0406; S06275; B31960; B21826
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-P
A:Reference number: JE0405
A:Accession: JE0406
A:Molecule type: DNA
A:Residues: 1-429 <RAH>
A:Cross-references: EMBL:X15227; NID:g18899; PIDD:CAA3299.1; PID:g295805
A:Experimental source: gene Amy56 for alpha-amylase
A:Genetics: A56
R:Rogers, J.C.
submitted to GenBank, September 1988
A:Reference number: A94535
A:Accession: B30759
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-104,'G',106-154,'A',156-160,'PD',163,'G',167-196,'V',198-342,'T',344-392,'
A:Cross-references: GB:J04202; NID:g166984; PIDD:AAA9615.1; PID:g166985
A:Experimental source: cv. Himalaya gene Amy46 for alpha-amylase B
A:Genetics: A46
R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
Plant Mol. Biol. 9, 3-17, 1987
A:Title: Structure and organization of two divergent alpha-amylase genes from barley.
A:Reference number: S06275
A:Accession: S06275
A:Molecule type: DNA
A:Residues: 1-11,'L',14-32,'S',34-57,'I',59-79,'Y',81-139,'R',141-160,'PA',163-164,'R',
A:Cross-references: EMBL:M17125; NID:g166978; PIDD:AAA32926.1; PID:g166979
A:Experimental source: cv. Sundance gene for alpha-amylase 1 precursor (clone p141.117)
A:Genetics: A41
A:Note: the authors translated the codon TCG for residue 33 as Trp
R:Khurshid, B.; Rogers, J.C.
J. Biol. Chem. 263, 18953-18960, 1988
A:Title: Barley alpha-amylase genes. Quantitative comparison of steady-state mRNA levels
A:Reference number: A92700; MUID:8506691; PMID:3264283
A:Accession: B31960
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-51 <KHD>
A:Experimental source: strain Himalaya gene Amy46 for alpha-amylase B precursor
R:Huang, J.K.; Swegle, M.; Dandekar, A.W.; Muthukrishnan, S.
J. Mol. Appl. Genet. 2, 579-588, 1984
A:Reference number: A92837; MUID:85159405; PMID:6335720
A:Accession: B21826
A:Molecule type: mRNA
A:Residues: 379-389,'T',391-392,'D',394-429 <HHA>
A:Cross-references: GB:R02636; NID:g166992; PIDD:AAA32932.1; PID:g166993
A:Experimental source: cv. Himalaya aleurone cell mRNA (clone 96 for alpha-amylase B)
C:Genetics: <A56>
A:Gene: Amy56
A:Introns: 29/3; 346/3
C:Genetics: <A46>
A:Gene: Amy46
C:Genetics: <AA1>
A:Gene: Amy1
A:Map position: 6
A:Introns: 29/3; 346/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; germination; glycosylase; hydrolase; polysaccharide degradati
F:172-318/Domain: alpha-amylase core homology <AMY>

```

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F:205,230,315/Active site: Asp, Glu, Asp #status predicted
Query Match 100.0%; Score 56; DB 1; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
DB 255 VNMVNRKVGGS 264

RESULT 2
ALRZOC
alpha-amylase (EC 3.2.1.1) precursor (clone O5Amy-c) - rice
C:Species: Oryza sativa (rice)
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 21-Jan-2000
C:Accession: S19142; PS0158
R:Kim, J.K.; Mu, R.
Plant Mol. Biol. 18, 399-402, 1992
A:Title: Nucleotide sequence of a high-pi rice (Oryza sativa) -amylase gene.
A:Reference number: S19142; MUID:92119260; PMID:1731997
A:Accession: S19142
A:Molecule type: DNA
A:Residues: 1-383 <KIM>
A:Cross-references: EMBL:X52240; NID:g20170; PIDD:CAA36485.1; PID:g20171
A:Experimental source: cv. IR26
R:Huang, N.; Kolzumi, N.; Rehl, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A:Title: Structural organization and differential expression of rice alpha-amylase ge
A:Reference number: J70945; MUID:91088278; PMID:2263460
A:Accession: PS0158
A:Molecule type: DNA
A:Residues: 1-50 <HDA>
A:Cross-references: GB:M59350; GB:M36983; NID:g169766; PIDD:AAA3893.1; PID:g169767
C:Genetics:
A:Introns: 31/3; 75/3; 313/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosylase; hydrolase; polysaccharide degradation
F:131/Domain: signal sequence #status predicted <SIG>
F:32-383/Product: alpha-amylase #status predicted <MAT>
F:150-289/Domain: alpha-amylase core homology <AMY>

Query Match 87.5%; Score 49; DB 1; Length 383;
Best Local Similarity 88.9%; Pred. No. 0.56;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 9
DB 226 VNMVNRKVGGS 234

RESULT 3
ALBH
alpha-amylase (EC 3.2.1.1) precursor - barley
C:Species: Hordeum vulgare (barley)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 18-Jun-1999
C:Accession: A00846; S65602
R:Rogers, J.C.; Millman, C.
J. Biol. Chem. 258, 8169-8174, 1983
A:Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
A:Reference number: A00846; MUID:8328423; PMID:6190808
A:Accession: A00846
A:Molecule type: mRNA
A:Residues: 1-438 <ROG>
A:Cross-references: GB:J01236; NID:g166986; PIDD:AAA32929.1; PID:g166987
A:Experimental source: cv. Himalaya
R:Unger, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B.
FEBS Lett. 363, 299-303, 1995
A:Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-
A:Reference number: S65602; MUID:9555567; PMID:7737421

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A:Accession: S65602
A:Molecule type: protein
A:Residues: 25-29 <TUG>
C:Comment: Production of this enzyme in barley is hormonally regulated. Germinating barl
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: calcium binding; glycosidase; hydrolase; monomer; polysaccharide degradation
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-438/Product: alpha sequence #status predicted <Sig>
F:171-316/Domain: alpha-amylase core homology <AMY>
F:204,229,313/Active site: Asp, Glu, Asp #status experimental

Query Match 85.7%; Score 48; DB 1; Length 438;
Best Local Similarity 80.0%; Pred. No. 0.95;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVGGS 10
||||:||||
DB 254 VNMVDRKVGGA 263

RESULT 4
ALBHB
alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; alpha-amylase 2
C:Species: Hordeum vulgare (barley)
C:Date: 30-Jun-1987 #sequence-revision 01-Sep-1995 #text-change 18-Jun-1999
C:Accession: A31960; A00847; J0405; A26267; A24457; A30759
R:Khurshheed, B.; Rogers, J.C.
J. Biol. Chem. 263:18953-18960, 1988
A:Title: Barley alpha-amylase genes: Quantitative comparison of steady-state mRNA levels
A:Reference number: A82700; M0ID:89066693; PMID:3264283
A:Accession: A31960
A:Molecule type: DNA
A:Residues: 1-427 <KH0>
A:Cross-references: GB:J04202
A:Experimental source: cv. Himalaya; gene Amy6-4
R:Rogers, J.C.
J. Biol. Chem. 260: 3731-3738, 1985
A:Title: Two barley alpha-amylase gene families are regulated differently in aleurone ce
A:Reference number: A00847; M0ID:85131184; PMID:3871776
A:Accession: A00847
A:Molecule type: mRNA
A:Residues: 1-133, 'D', 135-194, 'HRL', 198-424, 'Q', 426-427 <R0G>
A:Experimental source: seed
R:Rahmatullah, R.J.; Huang, J.K.; Clark, K.L.; Reeck, G.R.; Chandra, G.R.; Muthukrishnan
Plant Mol. Biol. 12, 119-121, 1989
A:Title: Nucleotide and predicted amino acid sequences of two different genes for high-F
A:Reference number: J0405
A:Accession: J0405
A:Molecule type: DNA
A:Residues: 1-133, 'D', 135-424, 'Q', 426-427 <RAH>
A:Cross-references: EMBL:X15226; NID:g18894; PIDN:CA33298.1; PID:g295804
A:Experimental source: gene Amy152
R:Chandler, P.M.; Zwar, J.A.; Jacobsen, J.V.; Higgins, T.J.V.; Inglis, A.S.
Plant Mol. Biol. 3, 407-418, 1984
A:Title: The effects of gibberellic acid and abscisic acid on alpha-amylase mRNA levels
A:Reference number: A26267
A:Accession: A26267
A:Molecule type: mRNA
A:Residues: 1-133, 'V', 135-184, 'A', 186-366, 'GA' <CHA>
A:Experimental source: cv. Himalaya
A:Note: the authors translated the codon GTC for residue 134 as Gly
R:Swenson, B.; Mundy, J.; Gibson, R.M.; Svendsen, I.
Carlsberg Res. Commun. 50, 15-22, 1985
A:Title: Partial amino acid sequences of alpha-amylase isozymes from barley malt.
A:Reference number: A24457
A:Accession: A24457
A:Molecule type: protein
A:Residues: 25-59, 'X', 61-67, 'HX', 70-85, 'X', 87-92, 'E', 94, 146-165, 228-251, 297-303, 'X', 305
C:Comment: The mRNA of this isozyme (B) is present at very low levels in unstimulated al

ed by the embryo during germination.
C:Genetics:
A:Gene: Amy2-2
A:Map position: 6
A:Inserts: 29/3; 344/3
A:Note: multigene family on chromosome 6 encodes type B alpha-amylases; type A alpha-
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: aleurone cell; blocked amino end; calcium binding; germination; glycosida
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-427/Product: alpha sequence #status predicted <AMY>
F:170-316/Domain: alpha-amylase core homology (in mature form) (probably pyrrolidone ca
F:203,228,313/Active site: Asp, Glu, Asp #status predicted

Query Match 83.9%; Score 47; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVG 9
||||:||||
DB 253 VNMVDRKVG 261

RESULT 5
S07040
alpha-amylase (EC 3.2.1.1) 2 precursor (clone p155.3) - barley
C:Species: Hordeum vulgare (barley)
C:Date: 28-Feb-1990 #sequence-revision 28-Feb-1990 #text-change 22-Jun-1999
C:Accession: S07040
R:Knox, C.A.P.; Sonthayanon, B.; Chandra, G.R.; Muthukrishnan, S.
Plant Mol. Biol. 9, 3-17, 1987
A:Title: Structure and organization of two divergent alpha-amylase genes from barley
A:Reference number: S06275
A:Accession: S07040
A:Molecule type: DNA
A:Residues: 1-437 <KNO>
A:Cross-references: EMBL:M17127; NID:g166982; PIDN:AAA3228.1; PID:g166983
C:Genetics:
A:Gene: amy2
A:Map position: 1
A:Inserts: 29/3; 74/1; 345/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:170-317/Domain: alpha-amylase core homology <AMY>
F:203,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 83.9%; Score 47; DB 2; Length 437;
Best Local Similarity 88.9%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNRKVG 9
||||:||||
DB 253 VNMVDRKVG 261

RESULT 6
S12625
alpha-amylase (EC 3.2.1.1) 3D - rice
C:Species: Oryza sativa (rice)
C:Date: 04-Dec-1992 #sequence-revision 04-Dec-1992 #text-change 22-Jun-1999
C:Accession: S12625; S12776; S15094; J03945
R:Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A:Title: Structural organization and differential expression of rice alpha-amylase ge
A:Reference number: J03945; M0ID:9108278; PMID:2263460
A:Accession: S12625
A:Molecule type: DNA

A:Residues: 1-435 <HUA>
 A:Cross-references: EMBL:M59351; NID:g169770; PIDD:AAA33895.1; PID:g169771
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in *Oryza sativa*: characterization of cDNA clones and mRNA
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12776
 A:Molecule type: mRNA
 A:Residues: 1-435 <ONE>
 A:Cross-references: EMBL:M24287
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
 Submitted to the EMBL Data Library, April 1989
 A:Description: The alpha-amylase genes in *Oryza sativa*: Characterization of cDNA clones
 A:Reference number: S15054
 A:Accession: S15054
 A:Molecule type: mRNA
 A:Residues: 1-72, 'R', '75-136, 'R', '138-435 <ON2>
 A:Cross-references: EMBL:M24287; NID:g169754; PIDD:AAA33886.1; PID:g169755
 A:Genetics: 30/3; 342/3
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-314/Domain: alpha-amylase core homology <AMY>
 F:203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 82.1%; Score 46; DB 2; Length 435;
 Best Local Similarity 88.9%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNAVGG 9
 |||||
 DB 253 VNMVNAVGG 261

RESULT 7
 UC7137
 alpha-amylase (EC 3.2.1.1) isozyme I - rice
 N:Alternate names: 1,4-gulcan glucanohydrolase I
 C:Species: *Oryza sativa* (rice)
 C>Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C:Accession: J07137; PC7039
 R:Abd, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
 Biosci. Biotechnol. Biochem. 63, 1329-1335, 1999
 A:Title: Characterization of chimeric enzymes constructed between two distinct alpha-amylase
 A:Reference number: J07137; MUID:99430781; PMID:10500994
 A:Accession: J07137
 A:Molecule type: mRNA
 A:Residues: 1-435 <ABE>
 A:Accession: PC7039
 A:Molecule type: protein
 A:Residues: 245-252 <AB2>
 C:Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages in
 is important in germinating seeds and is present as multiple isoforms.
 C:Genetics:
 A:Gene: amy-I
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 82.1%; Score 46; DB 2; Length 435;
 Best Local Similarity 88.9%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNAVGG 9
 |||||
 DB 253 VNMVNAVGG 261

RESULT 8
 S10013
 alpha-amylase (EC 3.2.1.1) 1 precursor (clone lambda-O8g2) - rice

C:Species: *Oryza sativa* (rice)
 C>Date: 21-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S10013
 R:Huang, N.; Sutliff, T.D.; Lits, J.C.; Rodriguez, R.L.
 Plant Mol. Biol. 14, 655-668, 1990
 A:Title: Classification and characterization of the rice alpha-amylase multigene faml
 A:Reference number: S10013; MUID:91346657; PMID:2102847
 A:Accession: S10013
 A:Molecule type: DNA
 A:Residues: 1-428 <HUA>
 A:Cross-references: EMBL:X16509; NID:g20166; PIDD:CAA34516.1; PID:g20167
 A:Experimental source: var. M202
 C:Genetics: 30/3; 75/1; 345/3
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:170-317/Domain: alpha-amylase core homology <AMY>

Query Match 80.4%; Score 45; DB 2; Length 428;
 Best Local Similarity 70.0%; Pred. No. 3.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNAVGG 10
 |||||
 DB 253 VNMVNAVGG 262

RESULT 9
 S12775
 alpha-amylase (EC 3.2.1.1) precursor (clone POS103) - rice
 C:Species: *Oryza sativa* (rice)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C:Accession: S12775
 R:O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.
 Mol. Gen. Genet. 221, 235-244, 1990
 A:Title: The alpha-amylase genes in *Oryza sativa*: characterization of cDNA clones and
 A:Reference number: S12775; MUID:90318322; PMID:2370848
 A:Accession: S12775
 A:Molecule type: mRNA
 A:Residues: 1-434 <ONE>
 A:Cross-references: EMBL:M24286; NID:g169752; PIDD:AAA33885.1; PID:g169753
 A:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:176-323/Domain: alpha-amylase core homology <AMY>
 F:209,234,320/Active site: Asp, Glu, Asp #status predicted

Query Match 80.4%; Score 45; DB 2; Length 434;
 Best Local Similarity 70.0%; Pred. No. 3.2;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNAVGG 10
 |||||
 DB 259 VNMVNAVGG 268

RESULT 10
 S14958
 alpha-amylase (EC 3.2.1.1) - rice
 C:Species: *Oryza sativa* (rice)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C:Accession: S14958
 R:Sutliff, T.D.; Huang, N.; Lits, J.C.; Rodriguez, R.L.
 Plant Mol. Biol. 16, 579-591, 1991
 A:Title: Characterization of an alpha-amylase multigene cluster in rice.
 A:Reference number: S14958; MUID:91329692; PMID:1714518
 A:Accession: S14958
 A>Status: translation not shown

A:Molecule type: DNA
 A:Residues: 1440 <SUN>
 A:Cross-references: EMBL:X56336; NID:g20334; PIDN:CAA39776.1; PID:g20335
 A:Genetics: 33/3; 78/1; 346/3
 A:Introns:
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:174-318/Domain: alpha-amylase core homology <AMY>
 F:207,232,315/Active site: Asp, Glu, Asp #status predicted

Query Match 75.0%; Score 42; DB 2; Length 440;
 Best Local Similarity 77.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

OY 1 VNMVKNVGG 9
 DB 257 VNMVKNVGG 265

RESULT 11
 H64206
 fructose-permease IIIC component frua homolog - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
 C:Accession: H64206
 R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uitterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.; C.A.; Venter, J.C.; Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; MUID:96026346; PMID:756993
 A:Accession: H64206
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues: 1-680 <TIGR>
 A:Cross-references: GB:U03685; GB:L43967; NID:g3844658; PIDN:AAC71279.1; PID:g1045736; T
 A:Experimental source: strain G-37
 A:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: phosphotransferase system enzyme II, fructose-specific; phosphotransferase

Query Match 75.0%; Score 42; DB 2; Length 680;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMVKNVGG 9
 DB 346 NMVKNVGG 353

RESULT 12
 S69535
 hypothetical protein 27 - phage HPI
 C:Species: phage HPI
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
 C:Accession: S69535
 R:Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scoocca, Nucleic Acids Res. 24, 2360-2368, 1996
 A:Title: The complete nucleotide sequence of bacteriophage HPI DNA.
 A:Reference number: S69503; MUID:96279738; PMID:8710508
 A:Accession: S69535
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-689 <ESP>
 A:Cross-references: EMBL:U24159; NID:g1046235; PIDN:AAB09214.1; PID:g1046256
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

Query Match 73.2%; Score 41; DB 2; Length 689;
 Best Local Similarity 75.0%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNVGG 9
 DB 166 NMVKNVGG 173

RESULT 13
 I36856
 B18L protein - variola virus
 N:Alternate names: B17L protein (COP)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
 C:Accession: I36856; S46875
 R:Blinov, V.M.
 submitted to Genbank, November 1992
 A:Reference number: A36859
 A:Accession: I36856
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <BLI>
 A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA49127.1; PID:g457077
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Koltyhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F. submitted to the EMBL Data Library April 1992
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H
 A:Reference number: S46868
 A:Accession: S46875
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <KOL>
 A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47527.1; PID:g516436
 A:Experimental source: strain India-1967, isolate Ind3
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNVGG 10
 DB 96 NMVKNVGG 104

RESULT 14
 T28614
 hypothetical protein B15L - variola major virus
 C:Species: variola major virus
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T28614
 R:Massing, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uitterback, T.R.; Koltyhalov, J.C.; Au Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <MAS>
 A:Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60924.1; PID:g439093
 A:Experimental source: strain Bangladesh 1975
 C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNVGG 10
 DB 96 NMVKNVGG 104

RESULT 15
 B72174
 D7L protein - variola minor virus (strain Garcia-1966)

C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 21-Jul-2000
C:Accession: B72174
R:Shchelkunov, S.N.; Tolmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopat
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: B72174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <SHC>
A:Cross-references: GB:Y16780; NID:q5830555; PIDN:CAB54788.1; PID:q5830749
A:Experimental source: strain garcia-1966
C:Genetics:
A:Gene: D7L
C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
|||:||||
DB 96 MWVSKVGDS 104

RESULT 16
T37451
probable 39.6K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Jun-2000
C:Accession: T37451
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL data library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
A:Reference number: Z20877
A:Accession: T37451
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <ANT>
A:Cross-references: EMBL:U94848; PIDN:AA96481.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA185L
C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
|||:||||
DB 96 MWVSKVGDS 104

RESULT 17
B17L protein - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 21-Jul-2000
C:Accession: G42527
R:Johnson, G.P.
submitted to GenBank, June 1990
A:Reference number: A33172
A:Accession: G42527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-340 <JOH>
C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;

Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
|||:||||
DB 96 MWVSKVGDS 104

RESULT 18
JQ1810
B16L protein - vaccinia virus (strain WR)
C:Species: vaccinia virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: JQ1810
R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A:Title: Nucleotide sequence of 42Kbp of vaccinia virus strain WR from near the right
A:Reference number: JQ1767; MID:91259063; PMID:2045793
A:Accession: JQ1810
A:Molecule type: DNA
A:Residues: 1-340 <SMI>
A:Cross-references: DDBJ:D11079; NID:q222717; PIDN:BAA01846.1; PID:q222761
C:Superfamily: vaccinia virus probable 39.6K protein

Query Match 71.4%; Score 40; DB 2; Length 340;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNVNRKVGGS 10
|||:||||
DB 96 MWVSKVGDS 104

RESULT 19
JQ1527
alpha-amylase (EC 3.2.1.1) 2A - rice
C:Species: Oryza sativa (rice)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 22-Jun-1999
C:Accession: JQ1527
R:Huang, N.; Rehl, S.J.; Rodriguez, R.L.
Gene 111, 223-228, 1992
A:Title: Rmy2A: a novel alpha-amylase-encoding gene in rice.
A:Reference number: JQ1527; MID:92175526; PMID:1541400
A:Accession: JQ1527
A:Molecule type: DNA
A:Residues: 1-443 <HUA>
A:Cross-references: GB:M74177; NID:q169768; PIDN:AAA33894.1; PID:q169769
C:Comment: Rice alpha-amylases are encoded by three multigene families, Amy1, Amy2
C:Genetics:
A:Gene: Rmy2A
A:Introns: 27/3; 71/1; 345/3
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:168-317/Domain: alpha-amylase core homology <AMT>
F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 71.4%; Score 40; DB 2; Length 443;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNVNRKVGGS 10
|:||||:
DB 253 VDWVDRVGGT 262

RESULT 20
S19990
alpha-amylase (EC 3.2.1.1) - rice
C:Species: Oryza sativa (rice)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999

C:Accession: S19990
 R:Goldman, S.; Mawl, Y.; Wu, R.
 Submitted to the EMBL Data Library, February 1992
 A:Reference number: S19990
 A:Accession: S19990
 A:Molecule type: mRNA
 A:Residues: 1-445 <GO>
 A:Cross-references: EMBL:X64619; NID:g20172; PIDN:CAA5903.1; PID:g20173
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:168-317/Domain: alpha-amylase core homology <AMY>
 F:202,228,314/Active site: Asp, Glu, Asp #status predicted

Query Match 71.4%; Score 40; DB 2; Length 445;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNMNRKVGCS 10
 DB 253 VDMVDRVGGT 262
 ||:|||||

RESULT 21
 VCLJBT
 env polyprotein precursor - bovine immunodeficiency virus (isolate 127)
 N:Alternate names: coat polyprotein
 N:Contains: coat protein gp40; coat protein gp62
 C:Species: bovine immunodeficiency virus
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-1997
 C:Accession: E34742
 R:Garvey, K.J.; Oberste, M.S.; Elser, J.E.; Braun, M.J.; Gonda, M.A.
 Virology 175, 391-409, 1990
 A:Title: Nucleotide sequence and genome organization of biologically active proviruses C
 A:Reference number: A34742; MUID:90223985; PMID:2183467
 A:Accession: E34742
 A:Molecule type: genomic RNA
 A:Residues: 1-904 <GAR>
 A:Cross-references: GB:M32690
 C:Genetics:
 A:Gene: env
 C:Superfamily: BIV env polyprotein
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
 F:1-13/Domain: signal sequence #status predicted <SIG>
 F:14-555/Product: coat protein gp62 #status predicted <GPI>
 F:556-904/Product: coat protein gp40 #status predicted <GPI>
 F:556-572/Domain: transmembrane #status predicted <TM1>
 F:729-747/Domain: transmembrane #status predicted <TM2>
 F:827-843/Domain: transmembrane #status predicted <TM3>
 F:131,235,277,296,329,367,385,410,427,432,452,491,509,541,597,663,694,877/Binding si

Query Match 71.4%; Score 40; DB 1; Length 904;
 Best Local Similarity 66.7%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVGCS 10
 DB 788 MNMNRKIGES 796
 ||:|||||

RESULT 22
 AG1312
 thioedoxin homolog lmo1903 [imported] - Listeria monocytogenes (strain EGD-e)
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1312
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgelet, O.; Entlian, K.D.; Fshih, H.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kun, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tleriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1312
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAC39981.1; PID:g16411356; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo1903

Query Match 69.6%; Score 39; DB 2; Length 157;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVG 9
 DB 146 MNMNRKVS 153
 ||:|||||

RESULT 23
 AG1684
 thioedoxin homolog lln2017 [imported] - Listeria innocua (strain Clp11262)
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1684
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgelet, O.; Entlian, K.D.; Fshih,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kref, J.; Kun, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.;
 ok, C.; Schlueter, T.; Simoes, N.; Tleriez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-157 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CAC97247.1; PID:g16414518; GSPDB:GN00178
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lln2017

Query Match 69.6%; Score 39; DB 2; Length 157;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 MNMNRKVG 9
 DB 146 MNMNRKVS 153
 ||:|||||

RESULT 24
 H72668
 hypothetical protein APE0774 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
 C:Accession: H72668
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72668
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <RAW>
 A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAH79752.1; PID:d1043538; PID:g
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0774
 C:Superfamily: Aeropyrum pernix hypothetical protein APE0774

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Query Match          69.6%; Score 39; DB 2; Length 397;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
DB 167 LNMVRRIGG 175

RESULT 25
AF1231
alpha,alpha-phosphotrehalase homolog lmo1254 [imported] - Listeria monocytogenes (strain
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AF1231
R:Glaser, P.; Frangenul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitouram, A.; Ma
ok, C.; Schlieter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1231
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-548 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99332.1; PID:g16410670; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1254
C:Superfamily: alpha-glucosidase; alpha-amyase core homology

Query Match          69.6%; Score 39; DB 2; Length 548;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
DB 137 NMVSKFGGN 145

RESULT 26
S17828
nuclease S1 - Penicillium citrinum
C:Species: Penicillium citrinum
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jun-2000
C:Accession: S17828
R:Maekawa, K.; Tsunasawa, S.; Dibo, G.; Sakiyama, F.
Eur. J. Biochem. 200, 651-661, 1991
A:Title: Primary structure of nuclease PI from Penicillium citrinum.
A:Reference number: S17828; MUID:92007841; PMID:1915339
A:Accession: S17828
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-270 <MAE>
C:Superfamily: Penicillium citrinum nuclease S1

Query Match          67.9%; Score 38; DB 2; Length 270;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
DB 258 NMINEIHGS 266

RESULT 27
JE0408
3'-nucleotidase (EC 3.1.3.6) PA3 - Penicillium sp.
N:Alternate names: nuclease PA3
C:Species: Penicillium sp.

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C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000
C:Accession: JE0408; PS0153
R:Tabata, N.; Kazama, H.; Ohgi, K.; Irie, M.
Agric. Biol. Chem. 55, 461-469, 1991
A:Title: Primary structure of a nuclease (nuclease PA3) from a Penicillium sp.
A:Reference number: JE0408; MUID:91299282; PMID:1369324
A:Accession: JE0408
A:Molecule type: protein
A:Residues: 1-270 <TAB>
C:Superfamily: Penicillium citrinum nuclease S1
C:Keywords: glycoprotein; phosphoric monoester hydrolase; zinc
F;92,138,184,197/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match          67.9%; Score 38; DB 2; Length 270;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVKNKVG 10
DB 258 NMINEIHGS 266

RESULT 28
AI0930
probable LysR-family transcription regulatory protein SRY3708 [imported] - Salmonella
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AI0930
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
, S.; Mout, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AI0930
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-278 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09467.1; PID:g16504584; GSPDB:GN00176
C:Genetics:
A:Gene: SRY3708

Query Match          67.9%; Score 38; DB 2; Length 278;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VNMVKNKVG 9
DB 230 VNMANKKG 238

RESULT 29
S10514
alpha-amyase (EC 3.2.1.1) precursor - black gram
C:Species: Vigna mungo (black gram)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S10514; S61336; S40201; S61334
R:Yamauchi, D.; Minamikawa, T.
Nucleic Acids Res. 18, 4250, 1990
A:Title: Nucleotide sequence of cDNA for alpha-amyase from cotyledons of germinating
A:Reference number: S10514; MUID:90332425; PMID:2377468
A:Accession: S10514
A:Molecule type: mRNA
A:Residues: 1-421 <YAM>
A:Cross-references: EMBL:X53049; NID:g22059; PIDN:CAA37217.1; PID:g22060
A:Accession: S61336
A:Molecule type: protein
A:Residues: 24-31 <YAM>
R:Takeuchi, H.; Yamauchi, D.; Wada, S.; Minamikawa, T.
submitted to the EMBL Data Library, June 1993
A:Description: Nucleotide sequence of the alpha-amyase gene from Vigna mungo.

```

A:Reference number: S40201
 A:Accession: S40201
 A:Molecule type: DNA
 A:Residues: 1-421 <TRAK>
 A:Cross-references: EMBL:X73301; NID:g437944; PIDN:CAA51734.1; PID:g437945
 C:Genetics:

A:Introns: 28/3; 72/1; 340/3
 C:Function:

A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Superfamily: wheat alpha-amylase; alpha-amylase core homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation; seed
 F:1-23/domain: signal sequence #status predicted <Sig>
 F:24-421/Product: alpha-amylase #status experimental <MAT>
 F:168-312/domain: alpha-amylase core homology <AMY>
 F:201,226,309/Active site: Asp, Glu, Asp #status predicted

Query Match 67.9%; Score 38; DB 2; Length 421;
 Best Local Similarity 60.0%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNKVGGS 10
 ||||| ||:
 DB 251 VNMVESAGGA 260

RESULT 30

AD2161
 alkaline phosphatase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AD2161
 R:Kaneko, T.; Nakamura, Y.; Wolk, C. P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AD2161
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-627 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA074542.1; PID:g17131937; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al12843

Query Match 67.9%; Score 38; DB 2; Length 627;
 Best Local Similarity 55.6%; Pred. No. 79;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVKNKVGGS 9
 ::||| ||
 DB 486 ISMINKNGG 494

Search completed: August 29, 2003, 18:48:31
 Job time : 12.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:39:11 ; Search time 6.57143 Seconds

(without alignments)

71.562 Million cell updates/sec

Title: US-09-830-876-3

Percent score: 56

Sequence: 1 VNMVNVGGS 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
|------------|-------|-------------|--------------|-------|-------------|
| 1 | 56 | 100.0 | 429 | 1 | AMV6_HORVU |
| 2 | 49 | 87.5 | 383 | 1 | AMC1_ORRSA |
| 3 | 48 | 85.7 | 438 | 1 | AMV1_HORVU |
| 4 | 47 | 83.9 | 368 | 1 | AMV3_HORVU |
| 5 | 47 | 83.9 | 427 | 1 | AMV3_HORVU |
| 6 | 46 | 82.1 | 435 | 1 | AMV3_HORVU |
| 7 | 45 | 80.4 | 428 | 1 | AMV3_ORRSA |
| 8 | 42 | 75.0 | 440 | 1 | AMV3_ORRSA |
| 9 | 42 | 75.0 | 680 | 1 | AMV3_ORRSA |
| 10 | 41 | 73.2 | 273 | 1 | AROE_BUCAP |
| 11 | 41 | 73.2 | 689 | 1 | Y027_BPHH1 |
| 12 | 40 | 71.4 | 340 | 1 | VB17_VACCV |
| 13 | 40 | 71.4 | 340 | 1 | VB17_VACCV |
| 14 | 40 | 71.4 | 340 | 1 | VB17_VACCV |
| 15 | 40 | 71.4 | 443 | 1 | AMV2_ORRSA |
| 16 | 40 | 71.4 | 445 | 1 | AMV2_ORRSA |
| 17 | 40 | 71.4 | 875 | 1 | ENV_BIV06 |
| 18 | 40 | 71.4 | 904 | 1 | ENV_BIV06 |
| 19 | 38 | 67.9 | 270 | 1 | NUP3_PENCI |
| 20 | 38 | 67.9 | 278 | 1 | NUP3_PENCI |
| 21 | 38 | 67.9 | 278 | 1 | NUP3_PENCI |
| 22 | 38 | 67.9 | 278 | 1 | NUP3_PENCI |
| 23 | 38 | 67.9 | 278 | 1 | NUP3_PENCI |
| 24 | 38 | 67.9 | 278 | 1 | NUP3_PENCI |
| 25 | 37 | 66.1 | 1070 | 1 | RPOB_SPTOL |
| 26 | 37 | 66.1 | 1070 | 1 | RPOB_SPTOL |
| 27 | 37 | 66.1 | 1070 | 1 | RPOB_SPTOL |
| 28 | 36 | 64.3 | 321 | 1 | YBEP_HABIN |
| 29 | 36 | 64.3 | 437 | 1 | AMV3_ORRSA |
| 30 | 36 | 64.3 | 438 | 1 | AMV3_ORRSA |
| 31 | 36 | 64.3 | 561 | 1 | TREC_BACSU |
| 32 | 36 | 64.3 | 969 | 1 | RPOB_CHLTR |
| 33 | 36 | 64.3 | 1070 | 1 | RPOB_CHLTR |

| | | | | | | |
|-----|----|------|------|---|------------|--------------------|
| 34 | 36 | 64.3 | 1070 | 1 | RPOB_TOBAC | P06271 nicotiana t |
| 35 | 36 | 64.3 | 1072 | 1 | RPOB_OENHO | P06275 oenothera h |
| 36 | 36 | 64.3 | 2418 | 1 | SPCA_HUMAN | P02549 homo sapien |
| 37 | 35 | 62.5 | 264 | 1 | MURI_STR3 | O86377 streptococ |
| 38 | 35 | 62.5 | 264 | 1 | MURI_STR5 | O86492 streptococ |
| 39 | 35 | 62.5 | 367 | 1 | S881_YEAST | P40073 saccharomyc |
| 40 | 35 | 62.5 | 373 | 1 | SERC_BUCBP | P59492 buchnera ap |
| 41 | 35 | 62.5 | 413 | 1 | AMV3_HHEAT | P08117 triticum ae |
| 42 | 35 | 62.5 | 440 | 1 | TIOB_HUMAN | O14763 homo sapien |
| 43 | 35 | 62.5 | 551 | 1 | TREC_ECOLI | P28904 escherichia |
| 44 | 35 | 62.5 | 569 | 1 | PLST_HUMAN | O14763 homo sapien |
| 45 | 35 | 62.5 | 627 | 1 | PLST_MOUSE | P13796 homo sapien |
| 46 | 35 | 62.5 | 627 | 1 | PLST_MOUSE | O61233 mus musculu |
| 47 | 35 | 62.5 | 627 | 1 | PLST_MOUSE | O61233 mus musculu |
| 48 | 35 | 62.5 | 627 | 1 | PLST_MOUSE | O61233 mus musculu |
| 49 | 35 | 62.5 | 627 | 1 | PLST_MOUSE | O61233 mus musculu |
| 50 | 35 | 62.5 | 629 | 1 | PLST_MOUSE | O61233 mus musculu |
| 51 | 35 | 62.5 | 630 | 1 | PLST_MOUSE | O61233 mus musculu |
| 52 | 35 | 62.5 | 769 | 1 | PLST_MOUSE | O61233 mus musculu |
| 53 | 35 | 62.5 | 770 | 1 | PLST_MOUSE | O61233 mus musculu |
| 54 | 35 | 62.5 | 809 | 1 | PLST_MOUSE | O61233 mus musculu |
| 55 | 35 | 62.5 | 891 | 1 | PLST_MOUSE | O61233 mus musculu |
| 56 | 35 | 62.5 | 938 | 1 | PLST_MOUSE | O61233 mus musculu |
| 57 | 35 | 62.5 | 968 | 1 | PLST_MOUSE | O61233 mus musculu |
| 58 | 34 | 60.7 | 122 | 1 | HY3A_HUMAN | O83622 buchnera ap |
| 59 | 34 | 60.7 | 126 | 1 | BBFA_TREPA | P01762 homo sapien |
| 60 | 34 | 60.7 | 199 | 1 | IL11_HUMAN | O83622 buchnera ap |
| 61 | 34 | 60.7 | 240 | 1 | SPSA_AERPE | P20809 homo sapien |
| 62 | 34 | 60.7 | 365 | 1 | C713_SOLME | O94147 aeropyrum p |
| 63 | 34 | 60.7 | 448 | 1 | SYC_IACLA | P37119 solanum mel |
| 64 | 34 | 60.7 | 507 | 1 | C714_SOLME | O94147 aeropyrum p |
| 65 | 34 | 60.7 | 567 | 1 | MA11_APIME | O94147 aeropyrum p |
| 66 | 34 | 60.7 | 702 | 1 | AD43_TENST | O17058 solanum mel |
| 67 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 68 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 69 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 70 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 71 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 72 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 73 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 74 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 75 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 76 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 77 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 78 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 79 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 80 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 81 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 82 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 83 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 84 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 85 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 86 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 87 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 88 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 89 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 90 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 91 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 92 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 93 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 94 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 95 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 96 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 97 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 98 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 99 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |
| 100 | 34 | 60.7 | 716 | 1 | AD43_TENST | O17058 solanum mel |

ALIGNMENTS

AMT6_HORVU STANDARD; PRT; 429 AA.
 ID AMT6_HORVU
 AC P04750;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clones GRAM56 and 963).
 GN AMY1.6.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OC Triticeae; Hordeum.
 NC NCBL_TaxID=4513;
 RN [1]
 RA "SEQUENCE FROM N.A. (CLONE GRAM56)."
 RA Rahmatullah R.J., Huang J.-K., Clark K.L., Reeck G.R.,
 RA Chandra G.R., Muthukrishnan S.;
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pI alpha-amylases from barley.";
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RX "SEQUENCE OF 380-429 FROM N.A. (CLONE 963)."
 RX MEDLINE=85159405; PubMed=6335720;
 RA Huang J.-K., Sweigle M., Dandekar A.M., Muthukrishnan S.;
 RT "Expression and regulation of alpha-amylase gene family in barley aleurones.";
 RL J. Mol. Appl. Genet. 2:579-588(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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 CC EMBL: X15227; CA33299.1; -
 CC EMBL: K02636; AAA32932.1; -
 CC PIR: J0406; J0406.
 CC HSSP: P04063; IAVA.
 CC InterPro: IPR006589; Alp_amy1_cat_sub.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC Pfam: PF00128; alpha-amylase: 1.
 CC SMART: SM00642; Amyy: 1.
 CC Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL
 FT CHAIN 1 24
 FT ACT_SITE 25 429 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 SQ SEQUENCE 429 AA; 47937 MW; 1C924CA6319D5262 CRC64;

Query Match 100.0%; Score 56; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVKNVGGG 10
 DB 255 VNMVKNVGGG 264

RESULT 2
 ID AMCL_ORYSA STANDARD; PRT; 383 AA.
 AC P27940;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-amylase isozyme C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B).
 GN Oryza sativa (Rice).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; OC Euphorbiaceae; Oryzae; Oryza.
 NC NCBL_TaxID=4530;
 RN [1]
 RA "SEQUENCE FROM N.A."
 RA STRAIN=cv. Indica-IR26; TISSUE=Leaf;
 RX MEDLINE=92119260; PubMed=1731997;
 RA Kim J.-K., Wu R.;
 RT "Nucleotide sequence of a high-pI rice (Oryza sativa) -amylase gene.";
 RL Plant Mol. Biol. 18:399-402(1992).
 RN [2]
 RX "SEQUENCE OF 1-50 FROM N.A."
 RX STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91088278; PubMed=2263460;
 RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
 RT "Structural organization and differential expression of rice alpha-amylase genes.";
 RL Nucleic Acids Res. 18:7007-7014(1990).
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING GERMINATION.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: IN CALLUS, WEAKLY EXPRESSED.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONE CELLS UNDER THE CONTROL OF THE PLANT HORMONE GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC CAUTION: ALL THE CATALYTIC RESIDUES ARE HIDDEN BY WHAT SEEMS TO BE FRAMESHIFT ERRORS FROM THE ORIGINAL NUCLEOTIDE REFERENCE.
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 CC EMBL: X52240; CA36485.1; -
 CC EMBL: M59350; AAA33893.1; -
 CC PIR: S19142; ALR20C.
 CC HSSP: P04063; IAVA.
 CC Gramene: P27940;
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
 KW Multigene family.
 FT SIGNAL
 FT CHAIN 1 31
 FT ACT_SITE 32 383 POTENTIAL.
 FT ACT_SITE 383 383 ALPHA-AMYLASE ISOZYME C.
 SQ SEQUENCE 383 AA; 43254 MW; 7426B9BE7C411B54 CRC64;

Query Match 87.5%; Score 49; DB 1; Length 383;
 Best Local Similarity 88.9%; Pred. No. 0.22;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNVGG 9
 DB 226 VNMVKNVGG 234

RESULT 3
 ID AMY3_HORVU STANDARD; PRT; 438 AA.
 AC P00693;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY1) (low pI alpha-amylase).
 GN AMY1.3.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cy Himalaya;
 RX MEDLINE=61328423; PubMed=6190808;
 RA Rogers J.C., Millman C.;
 RT Isolation and sequence analysis of a barley alpha-amylase cDNA clone.";
 RL J. Biol. Chem. 258:8169-8174(1983).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: J01236; AAA32929.1; -.
 DR EMBL: J01236; AAA32929.1; -.
 DR PIR: A00846; ALBH.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_ami1_cat_sub.
 DR InterPro: IPR006047; Alpha_ami1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 1 24
 FT ACT_SITE 25 438 ALPHA-AMYLASE TYPE A ISOZYME.
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT ACT_SITE 229 229 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 FT NON_TER 368 368
 SQ SEQUENCE 438 AA; 47796 MW; 2393FDC5180F51 CRC64;

Query Match 85.7%; Score 48; DB 1; Length 438;
 Best Local Similarity 80.0%; Pred. No. 0.38;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 VNMVKNVGG 10
 |||||:||||

DB 254 VNMVKNVGG 263

RESULT 4
 ID AMY3_HORVU STANDARD; PRT; 368 AA.
 AC P04747;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Clone PHV19) (Fragment).
 GN AMY1.3.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Chandler P.M., Zwart J.A., Jacobsen J.V., Higgins T.J.V., Inglis A.S.;
 RT "The effects of gibberellin acid and abscisic acid on alpha amylase mRNA levels in barley aleurone layers studies using an alpha amylase cDNA clone.";
 RL Plant Mol. Biol. 3:407-418(1984).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS HORMONALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELLIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- MISCELLANEOUS: TYPE B ISOZYME mRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELLIC ACID.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: K02638; AAA2933.1; -.
 DR EMBL: K02638; AAA2933.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006589; Alp_ami1_cat_sub.
 DR InterPro: IPR006047; Alpha_ami1_cat.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal.
 FT SIGNAL 1 24
 FT CHAIN 1 24
 FT ACT_SITE 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 203 203 BY SIMILARITY.
 FT ACT_SITE 228 228 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT NON_TER 368 368
 SQ SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;

Query Match 83.9%; Score 47; DB 1; Length 368;
 Best Local Similarity 88.9%; Pred. No. 0.49;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 VNMVKNVGG 9
 |||||:||||

DB 253 VNMVKNVGG 261

RESULT 5
 ID AMY2_HORVU STANDARD; PRT; 427 AA.
 AC P04063;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase).
 GN AMY1.2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rahmatullah R.J., Huang J.K., Clark K.L., Reek G.R.,
 RA Chandra G.R., Muthukrishnan S.,
 RT "Nucleotide and predicted amino acid sequences of two different genes for high-pI alpha-amylases from barley.";
 RL Plant Mol. Biol. 12:119-121(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85131184; PubMed=3871776;
 RA Rogers J.C.,
 RT "Two barley alpha-amylase gene families are regulated differently in aleurone cells.";
 RL J. Biol. Chem. 260:3731-3738(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RA MEDLINE=94234083; PubMed=8196040.
 RA Kadziola A., Abe J.-I., Svensson B., Haser R.,
 RT "Crystal and molecular structure of barley alpha-amylase.";
 RL J. Mol. Biol. 239:104-121(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF COMPLEX WITH BASI.
 RC STRAIN=cv. Mennet;
 RX MEDLINE=98298441; PubMed=9634702;
 RA Vallee F., Kadziola A., Bourne Y., Juy M., Rodenburg K.W.,
 RA Svensson B., Haser R.,
 RT "Barley alpha-amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9-A resolution.";
 RL Structure 6:649-659(1998).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- DEVELOPMENTAL STAGE: PRODUCTION OF ALPHA-AMYLASE IS NORMALLY REGULATED. GERMINATING EMBRYOS PRODUCE THE HORMONE GIBBERELIC ACID, WHICH WITHIN 10 HOURS STIMULATES THE ALEURONE CELLS COVERING THE ENDOSPERM OF THE SEED TO PRODUCE ALPHA-AMYLASE. THE ENZYME THEN DEGRADES THE STARCH WITHIN THE ENDOSPERM FOR USE BY THE DEVELOPING PLANT EMBRYO.
 CC -1- INDUCTION: TYPE B ISOZYME MRNA IS UNDETECTABLE IN UNSTIMULATED CELLS AND INCREASES A HUNDRED-FOLD AFTER STIMULATION WITH GIBBERELIC ACID.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; X15226; CAA33298.1; -;
 CC EMBL; K02637; AAA98790.1; -;

DR PIR; A31960; ALBHB.
 DR PDB; LAMY; 13-MAY-95.
 DR PDB; IAVA; 16-MAR-99.
 DR PDB; IBG9; 15-JUN-99.
 DR InterPro; IP006589; Alp_amy1_cat.sub.
 DR InterPro; IP006047; Alpha_amy1_cat.
 DR InterPro; IP006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR HydroLase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 427
 FT ACT_SITE 203 203
 FT ACT_SITE 228 228
 FT ACT_SITE 313 313
 FT CONFLICT 134 134
 FT CONFLICT 195 197
 FT CONFLICT 425 425
 FT STRAND 27 29
 FT STRAND 33 34
 FT STRAND 35 37
 FT STRAND 39 40
 FT HELIX 42 47
 FT HELIX 48 49
 FT TURN 50 56
 FT TURN 57 57
 FT STRAND 60 63
 FT STRAND 69 69
 FT TURN 72 73
 FT STRAND 77 77
 FT TURN 80 81
 FT TURN 84 85
 FT TURN 87 88
 FT TURN 91 104
 FT TURN 105 105
 FT STRAND 107 112
 FT STRAND 116 116
 FT STRAND 121 122
 FT STRAND 124 125
 FT STRAND 128 130
 FT TURN 139 140
 FT TURN 144 146
 FT HELIX 147 147
 FT STRAND 149 150
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 FT STRAND 165 165
 FT TURN 168 169
 FT STRAND 172 173
 FT TURN 175 176
 FT HELIX 178 193
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 FT HELIX 205 207
 FT HELIX 210 220
 FT STRAND 224 227
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 FT STRAND 237 238
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 FT STRAND 246 260
 FT HELIX 261 262
 FT TURN 265 268
 FT STRAND 270 279
 FT HELIX 280 282
 FT HELIX 284 287
 FT TURN 290 291
 FT HELIX 297 299
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 FT TURN 302 304
 FT HELIX 305 308
 FT STRAND 312 314


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FT TURN 316 318
FT HELIX 325 327
FT HELIX 328 337
FT STRAND 341 345
FT HELIX 346 350
FT TURN 351 351
FT HELIX 355 357
FT TURN 368 369
FT TURN 372 373
FT STRAND 376 382
FT TURN 383 384
FT STRAND 385 390
FT TURN 391 393
FT STRAND 394 398
FT HELIX 405 407
FT STRAND 412 418
FT TURN 419 420
FT STRAND 421 427
SQ SEQUENCE 427 AA; 47355 MW; 957C0B1621BF748 CRC64;

Query Match 83.9%; Score 47; DB 1; Length 427;
Best Local Similarity 88.9%; Pred. No. 0.56;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVNAKVG 9
Db 253 VNMVNAKVG 261

RESULT 6
AM3D_ORYSA STANDARD; PRT; 435 AA.
ID AM3D_ORYSA
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriharoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; Tissue=Etolated leaf;
RX MEDLINE=91088728; PubMed=2263460.
RA Huang N., Koiwumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
RT amylase genes."
RL Nucleic Acids Res. 18:7007-7014(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848.
RA O'Neill S.D., Kumagai M.H., Majumdar A., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL TISSUES, EXCEPT IN
CC IMMATURE SEEDS. IS THE MOST ABUNDANT ALPHA-AMYLASE ISOZYME IN
CC CALLUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

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CC -----
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: M59351; AAA33895.1; -
DR EMBL: M24287; AAA33886.1; -
DR PIR: S12625; S12625.
DR HSP: P04063; IAVA.
DR Gramene: P27933; -
DR InterPro: IPR006589; Alp_aml1_cat_sub.
DR InterPro: IPR006047; Alp_aml1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amyy; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1..25
FT CHAIN 26..435
FT ACT_SITE 203..203
FT ACT_SITE 311..311
FT METAL 116..116
FT METAL 174..174
FT CONFLICT 73..74
FT CONFLICT 137..137
SQ SEQUENCE 435 AA; 47911 MW; 1BB06A195BA0D6 CRC64;

Query Match 82.1%; Score 46; DB 1; Length 435;
Best Local Similarity 88.9%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VNMVNAKVG 9
Db 253 VNMVNAKVG 261

RESULT 7
AMYL_ORYSA STANDARD; PRT; 428 AA.
ID AMYL_ORYSA
AC P17654;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (Isozyme 1b).
GN AMY1.1 OR AMY1A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriharoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202;
RX MEDLINE=91346657; PubMed=2102847;
RA Huang N., Sutliff T.D., Lits J.C., Rodriguez R.L.;
RT "Classification and characterization of the rice alpha-amylase
RT multigene family."
RL Plant Mol. Biol. 14:655-668(1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS103).
RX STRAIN=cv. Japonica M202;
RX MEDLINE=90318322; PubMed=2370848.
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
RT clones and mRNA expression during seed germination."
RL Mol. Genet. 221:235-244(1990).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING

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CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MORE ABUNDANT IN GERMINATING SEEDS, THAN IN
CC CALLUS, YOUNG ROOTS AND LEAVES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- PPM: ONLY CEREAL AMYLASE KNOWN TO BE GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X16509; CAA34516.1; -.
DR PIR: S10013; S10013.
DR HSP: P04063; IAVA.
DR Gramene; P17654; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR HydroLase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Glycoprotein; Multigene family.
FT SIGNAL 1 25 PROBABLE.
FT CHAIN 26 428 ALPHA-AMYLASE.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 116 116 CALCIUM (BY SIMILARITY).
FT METAL 174 174 CALCIUM (BY SIMILARITY).
FT CARBOHND 265 265 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 428 AA; 4775 MW; 3B71403AACF6C6A6 CRC64;

Query Match 80.4%; Score 45; DB 1; Length 428;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNMVNRKVGGS 10
Db 253 VNMVDRVGA 262

RESULT 8
AM3A_ORYSA STANDARD; PRT; 440 AA.
ID AM3A_ORYSA
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan 4-glucohydrolase).
GN AM1.2 OR AM3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;

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RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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CC -----
DR EMBL: X56336; CAA39776.1; -.
DR PIR: S14958; S14958.
DR HSP: P04063; IAVA.
DR Gramene; P27932; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR HydroLase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 440 ALPHA-AMYLASE ISOZYME 3A.
FT ACT_SITE 207 207 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
FT METAL 119 119 CALCIUM (BY SIMILARITY).
FT METAL 178 178 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;

Query Match 75.0%; Score 42; DB 1; Length 440;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNMVNRKVG 9
Db 257 VNMVNRKVG 265

RESULT 9
PTFA_MYCGE STANDARD; PRT; 680 AA.
ID PTFA_MYCGE
AC P47308;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE PFS system, fructose-specific IIAB component (EIIBC-Fru) (Fructose-
DE permease IIAB component) (Phosphotransferase enzyme II, ABC
DE component) (EC 2.7.1.69) (EII-Fru/EIII-Fru).
GN PTFA OR MG062.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OC Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.;

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RA Nguyen D.T., Uterback T.R., Saudak D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bolt K.F., Hu P.-C., Luchter T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT The minimal genome complement of *Mycoplasma genitalium*.
 RL Science 270:397-403(1995).
 RN [2]
 RN SEQUENCE OF 147-253 FROM N.A.
 RC STRAIN-ATCC 33530 / G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bolt K.F., Hutchison C.A. III;
 RT "A survey of the *Mycoplasma genitalium* genome by using random
 RT sequencing."
 RL J. Bacteriol. 175:7918-7930(1993).
 RN [3]
 RN DISCUSSION OF SEQUENCE.
 RP MEDLINE=98353635; PubMed=9689210;
 RA Reizer J., Paulsen I.T., Reizer A., Tilgemyer F., Sajer M.H. Jr.;
 RT "Novel phosphotransferase system genes revealed by bacterial genome
 RT analysis: the complete complement of pts genes in *Mycoplasma
 RT genitalium*."
 RL Microb. Comp. Genomics 1:151-164(1996).
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
 CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS). A MAJOR CARBOHYDRATE ACTIVE
 CC -TRANSPORT SYSTEM. THE TCD DOMAIN CONTAIN THE SUGAR BINDING SITE
 CC AND THE TRANSMEMBRANE CHANNEL. THE IIA DOMAIN CONTAINS THE PRIMARY
 CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
 CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
 CC THE SUGAR.
 CC -1- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
 CC histidine + sugar phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Contains 1 PTS_EIIA domain.
 CC -1- SIMILARITY: Contains 1 PTS_EIIB domain.
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 CC -----
 DR EMBL: U03685; AAC71279.1; -
 DR EMBL: U02138; AAD12415.1; -
 DR PIR: H64206; H64206.
 DR TIGR: MG062; -
 DR InterPro: IPR002178; PTS_EIIA_2.
 DR InterPro: IPR003352; PTS_EIIC.
 DR InterPro: IPR003353; PTS_IIB-fruc.
 DR InterPro: IPR006327; PTS_IIC-fruct.
 DR InterPro: IPR004715; PTSIIA-fruc.
 DR Pfam: PF00359; PTS_EIIA_2; 1.
 DR Pfam: PF02378; PTS_EIIC; 1.
 DR Pfam: PF02379; PTS_IIB-fruc; 1.
 DR ProDom: PD001689; PTS_EIIA_2; 1.
 DR TIGRFAMs: TIGR00829; FRU; 1.
 DR TIGRFAMs: TIGR00848; frua; 1.
 DR TIGRFAMs: TIGR01427; PTS_IIC-fructo; 1.
 DR TIGRFAMs: TIGR01427; PTS_IIC-fructo; 1.
 KM Phosphotransferase system: Sugar transport; Transferase;
 KM Phosphorylation; Transmembrane; Complete proteome.
 FT DOMAIN 1 68
 FT DOMAIN ? 680
 FT MOD_RES ? 680
 FT MOD_RES 174 174
 FT MOD_RES 306 326
 FT TRANSMEM 352 372
 FT TRANSMEM 377 397
 FT TRANSMEM 410 430
 FT TRANSMEM 449 469
 FT TRANSMEM 488 508
 FT TRANSMEM 532 552
 FT TRANSMEM POTENTIAL.
 FT TRANSMEM POTENTIAL.

FT TRANSMEM 565 585 POTENTIAL.
 FT TRANSMEM 590 610 POTENTIAL.
 FT TRANSMEM 618 638 POTENTIAL.
 FT TRANSMEM 643 663 POTENTIAL.
 SQ SEQUENCE 680 AA; 74090 MW; 56AC1BD7AA9D4 CRC64;
 Query Match 75.0%; Score 42; DB 1; Length 680;
 Best Local Similarity 75.0%; Pred. No. 6.6;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 MWNVKVG 9
 Db 346 MWLNLKLG 353
 |||:|:
 |||:|:
 RESULT 10
 ID AROE_BUCAP STANDARD; PRT; 273 AA.
 AC P46240;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Shikimate 5-dehydrogenase (EC 1.1.1.25).
 GN AROE OR BUSC474
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95212914; PubMed=7535281;
 RA Roubaksh D., Baumann P.;
 RT "Characterization of a putative 23S-5S rRNA operon of *Buchnera
 RT aphidicola* (endosymbiont of aphids) unlinked to the 16S rRNA-encoding
 RT gene."
 RL Gene 155:107-112(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tams J., Klasson L., Canbaek B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria".
 RL Science 296:2376-2379(2002).
 CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
 CC NADPH.
 CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC fourth step.
 CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL: U09230; AAD09433.1; -
 DR EMBL: AE014124; AAM68017.1; -
 DR HAMAP: MF_00222; ? 1.
 DR InterPro: IPR006152; Shikimate.
 DR InterPro: IPR006151; Shikimate_DH.
 DR Pfam: PF01488; Shikimate_DH; 1.
 DR TIGRFAMs: TIGR00507; AROE; 1.
 KM Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
 KM Complete proteome.
 FT CONFLICT 203 204 LP -> T (IN REF. 1).
 FT CONFLICT 206 206 S -> I (IN REF. 1).
 FT CONFLICT 212 212 T -> R (IN REF. 1).
 SQ SEQUENCE 273 AA; 30885 MW; 50507AF854774A6 CRC64;
 Query Match 73.2%; Score 41; DB 1; Length 273;
 Best Local Similarity 60.0%; Pred. No. 4.3;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NMVNVKVGGS 10
: || : | |||
Db 227 INMCKRAGGS 236

RESULT 11
YO27_BPBP1 STANDARD; PRT; 689 AA.
ID YO27_BPBP1 STANDARD; PRT; 689 AA.
AC P51731;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 72.8 kDa protein in Lys 3 region (ORF27).
OS Bacteriophage HP1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=10690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HP1C1;
RX MEDLINE=85128433; PubMed=6098523;
RA Benjamin R.C., Fitzmaurice W.P., Huang P.C., Scocca J.J.;
RT "Nucleotide sequence of cloned DNA segments of the Haemophilus
RT Influenzae bacteriophage HP1C1."
RL Gene 31:173-185(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HP1C1;
RX MEDLINE=96279738; PubMed=8710508;
RA Esposito D., Fitzmaurice W.P., Benjamin R.C., Goodman S.D.,
RA Waldman A.S., Scocca J.J.;
RT "The complete nucleotide sequence of bacteriophage HP1 DNA."
RL Nucleic Acids Res. 24:2360-2368(1996).
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CC
CC EMBL: U24159; AAB09214.1; -
DR PIR: S69535; S69535.
RW Hypothetical protein; Transmembrane.
FT TRANSMEM 385 405 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
SQ SEQUENCE 689 AA; 72837 MW; CCDDBBACAI7C22 CRC64;
Query Match 73.2%; Score 41; DB 1; Length 689;
Best Local Similarity 73.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 9
: ||||| : |
Db 166 NMVNVKING 173

RESULT 12
VB17_VACCC STANDARD; PRT; 340 AA.
ID VB17_VACCC STANDARD; PRT; 340 AA.
AC P21075;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein B17.
GN B17L.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10249;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus."
RL Virology 179:247-266(1990).
RN [2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'";
RL Virology 179:517-563(1990).
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CC
CC EMBL: M35027; AAA48216.1; -
DR PIR: G42527; G42527.
SQ SEQUENCE 340 AA; 39505 MW; 11B23AE072A4EF CRC64;
Query Match 71.4%; Score 40; DB 1; Length 340;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 10
: ||||| : |
Db 96 NMVNVKVGDS 104

RESULT 13
VB17_VACCV STANDARD; PRT; 340 AA.
ID VB17_VACCV STANDARD; PRT; 340 AA.
AC 001221;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Protein B17.
GN B17L OR B16L.
OS Vaccinia virus (strain WR).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91259063; PubMed=2045793;
RA Smith G.L., Chan Y.S., Howard S.T.;
RT "Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RT the right inverted terminal repeat."
RL J. Gen. Virol. 72:1349-1376(1991).
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CC
CC EMBL: D11079; BAA01846.1; -
DR PIR: J01810; J01810.
SQ SEQUENCE 340 AA; 39565 MW; 52680AA44C249AC9 CRC64;
Query Match 71.4%; Score 40; DB 1; Length 340;
Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NMVNVKVGGS 10
: ||||| : |

```

Db          96 NMVSKVGS 104

RESULT 14
VBI7_VARY STANDARD; PRT: 340 AA.
AC P33876;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Protein B17.
GN B17L OR B18L OR B15L.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-India-1967 / Isolate Ind3;
RX MEDLINE=92209372; PubMed=166548;
RA Shchelkunov S.N., Marenikova S.S., Tolmenin A.V., Blinov V.M.,
RA Chizhikov V.E., Gutorov V.V., Safronov P.F., Pozdnyakov S.G.,
RA Shelukhina E.M., Gashnikov P.V., Anjaparidze O.G., Sandakhchiev L.S.;
RT "Creation of a clone library of fragments from the natural variola
RT virus and study of the structural and functional organization of
RT viral genes from a circle of hosts".
RT Dokl. Akad. Nauk SSSR 321:402-406(1991).
RN [2]
RP COMPLETE GENOME.
RC STRAIN-India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384159;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.".
RT FEBS Lett. 319:80-83(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Maassung R.F., Esposito J.J., Liu L., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavang A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.".
RT Nature 366:748-751(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Somalia-1977, and Garcia-1966;
RA Maassung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Tolmenin A.V., Shchelkunov S.N., Esposito J.J.;
RT Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X69198; CA449127.1; -
DR EMBL: X67117; CA447527.1; -
DR EMBL: X72086; CA50968.1; -
DR EMBL: L22579; AA60924.1; -
DR EMBL: U18339; AA69397.1; -
DR EMBL: U18341; AA69457.1; -
DR PIR: B72174; B72174.
DR PIR: I36856; I36856.
DR PIR: T28614; T28614.
SQ SEQUENCE 340 AA; 39673 MW; 4C40C18C9CE692448 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 340;

Best Local Similarity 77.8%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db          2 NMVSKVGS 10
1111111111
96 NMVSKVGS 104

RESULT 15
AM2A_ORYSA STANDARD; PRT: 443 AA.
ID AM2A_ORYSA
AC P27935;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 2A precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.5 OR AMY2A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-cv Japonica M202;
RX MEDLINE=92175526; PubMed=1541400;
RA Huang Z., Reini S.J., Rodriguez R.L.;
RT "Amy2A: a novel alpha-amylase-encoding gene in rice.".
RT Gene 111:223-228(1992).
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: M74177; AA33894.1; -
DR PIR: J01527; J01527.
DR HSP: P04063; IAVA.
DR Gramene; P27935.
DR InterPro; IPR006047; Alpha_amy1-cat.
DR Pfam; PF00128; alpha-amylase; 1.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 443 POTENTIAL.
FT ACT_SITE 202 202 ALPHA-AMYLASE ISOZYME 2A.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 113 113 CALCIUM (BY SIMILARITY).
FT METAL 172 172 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 443 AA; 48527 MW; 7B3F9264404F67F6 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 443;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db          1 NMVSKVGS 10
1111111111
253 VDWWDVWGGR 262

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RESULT 16
AMC2_ORYSA STANDARD; PRT; 445 AA.
ID P27941
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme C2 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.8
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Indica-IR26; TISSUE=Seed;
RA Goldman S., Mawal Y., Wu R.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL: X64619; CAA45903.1; -.
DR PIR: S19980; S19990.
DR HSSP: P04063; IAVA.
DR Gramene: P27941; -.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR Pfam: PF00128; alpha-amylase; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; signal;
KW Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 445 ALPHA-AMYLASE ISOZYME C2.
FT ACT_SITE 202 202 BY SIMILARITY.
FT ACT_SITE 314 314 BY SIMILARITY.
FT METAL 113 113 CALCIUM (BY SIMILARITY).
FT METAL 172 172 CALCIUM (BY SIMILARITY).
SO SEQUENCE 445 AA; 49207 MW; DED23701E836ACDA CRC64;
Query Match 71.4%; Score 40; DB 1; Length 445;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENV polypeptide precursor (coat polypeptide) [contains: Coat protein
DE GP62; Coat protein GP40].
GN ENV.
OS Bovine immunodeficiency virus (isolate 106) (BIV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11658;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90223985; PubMed=2183467;
RA Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;
RT "Nucleotide sequence and genome organization of biologically active
RT proviruses of the bovine immunodeficiency-like virus.";
RL Virology 175:391-409(1990).
RN [2]
RP SEQUENCE OF 1-99 FROM N.A.
RX MEDLINE=91251255; PubMed=1645801;
RA Oberste M.S., Greenwood J.D., Gonda M.A.;
RT "Analysis of the transcription pattern and mapping of the putative
RT rev and env splice junctions of bovine immunodeficiency-like virus.";
RL J. Virol. 65:3932-3937(1991).
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CC -----
DR EMBL: M32691; NOT ANNOTATED_CDS.
DR EMBL: M74711; AAA42762.1; -.
DR HIV: M32691; ENVBIV106.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane; signal.
FT SIGNAL 1 13
FT CHAIN 14 555
FT CHAIN 556 875
FT TRANSMEM 694 722
FT CARBOHYD 131 131
FT CARBOHYD 248 248
FT CARBOHYD 267 267
FT CARBOHYD 300 300
FT CARBOHYD 338 338
FT CARBOHYD 347 347
FT CARBOHYD 356 356
FT CARBOHYD 381 381
FT CARBOHYD 398 398
FT CARBOHYD 403 403
FT CARBOHYD 423 423
FT CARBOHYD 462 462
FT CARBOHYD 480 480
FT CARBOHYD 512 512
FT CARBOHYD 568 568
FT CARBOHYD 634 634
FT CARBOHYD 665 665
FT CARBOHYD 848 848
FT CONFLICT 24 24
FT CONFLICT 92 92
SO SEQUENCE 875 AA; 99166 MW; EBE6FCB32747EA6C CRC64;
Query Match 71.4%; Score 40; DB 1; Length 875;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 17
ENV_BIV06 STANDARD; PRT; 875 AA.
ID ENV_BIV06
AC P19556;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

RESULT 18
ENV_BIV27 STANDARD; PRT; 904 AA.
ID ENV_BIV27
Db 759 NWLNKIGES 767

```

AC p19557;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENY Polypeptide precursor (Coat polypeptide) [contains: Coat protein
DE GP62; Coat protein GP40].
GN ENY.
OS Bovine immunodeficiency virus (isolate 127) (BIV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11659;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90223985; PubMed=2183467;
RA Garvey K.J., Oberste M.S., Elser J.E., Braun M.J., Gonda M.A.;
RT "Nucleotide sequence and genome organization of biologically active
RT proviruses of the bovine immunodeficiency-like virus.";
RL Virology 175:391-409(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M32690; AAA91274.1; -.
DR PIR: E34742; VCLJBT.
DR HIV: M32690; ENV5BIV127.
KW Glycoprotein; Coat protein; Polypeptide; Transmembrane; Signal.
FT SIGNAL 1 13
FT CHAIN 14 555
FT CHAIN 556 904
FT TRANSMEM 723 751
FT CARBOHYD 131 131
FT CARBOHYD 255 255
FT CARBOHYD 277 277
FT CARBOHYD 296 296
FT CARBOHYD 329 329
FT CARBOHYD 367 367
FT CARBOHYD 376 376
FT CARBOHYD 385 385
FT CARBOHYD 410 410
FT CARBOHYD 427 427
FT CARBOHYD 432 432
FT CARBOHYD 452 452
FT CARBOHYD 491 491
FT CARBOHYD 509 509
FT CARBOHYD 541 541
FT CARBOHYD 597 597
FT CARBOHYD 683 683
FT CARBOHYD 694 694
FT CARBOHYD 877 877
FT SEQUENCE 904 AA; 102269 MW; F56100HC2AECDD66F CRC64;

Query Match 71.4%; Score 40; DB 1; Length 904;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNRKGGGS 10
DB 788 NMLNRKIGES 796
11:11:11

RESULT 19
ID NUP1_PENCI STANDARD; PRT; 270 AA.
AC P24289;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclease P1 (PC 3.1.30.1) (Endonuclease P1) (Deoxyribonuclease P1).
OS Penicillium citrinum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5077;
RN [1]
RP SEQUENCE.
RX MEDLINE=92007841; PubMed=1915339;
RA Maekawa K., Tsunashima S., Dibo G., Sakiyama F.;
RT "Primary structure of nuclease P1 from Penicillium citrinum.";
RL Eur. J. Biochem. 200:651-661(1991).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=91266887; PubMed=1710977;
RA Volbeda A., Lahm A., Sakiyama F., Suck D.;
RT "Crystal structure of Penicillium citrinum P1 nuclease at 2.8-A
RT resolution.";
RL EMBO J. 10:1607-1618(1991).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS);
RX MEDLINE=98393014; PubMed=9726413;
RA Komler G., Dominguez R., Lahm A., Dahl O., Suck D.;
RT "Recognition of single-stranded DNA by nuclease P1: high resolution
RT crystal structures of complexes with substrate analogs.";
RL Protein 32:414-424(1998).
CC -1- FUNCTION: Hydrolyzes only single stranded DNA and RNA without
CC apparent specificity for bases.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC -1- phosphomononucleotide and 5'-phosphooligonucleotide end-products.
CC -1- COFACTOR: BINDS 3 ZINC IONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO A.ORYZAE NUCLEASE S1, AND BARLEY NUCLEASE.
DR PIR: S17828; S17828.
DR PDB: 1AK0; 03-DEC-97.
DR InterPro: IPR003154; S1/P1nuclease.
KW P1nuclease; Nuclease; Endonuclease; Glycoprotein; Zinc; 3D-structure.
FT DISULFID 72 217
FT CARBOHYD 80 85
FT CARBOHYD 92 92
FT CARBOHYD 138 138
FT CARBOHYD 184 184
FT CARBOHYD 197 197
FT METAL 1 1
FT METAL 6 6
FT METAL 45 45
FT METAL 60 60
FT METAL 116 116
FT METAL 120 120
FT METAL 126 126
FT METAL 149 149
FT METAL 153 153
FT METAL 270 270
FT HELIX 3 16
FT HELIX 19 29
FT HELIX 30 30
FT HELIX 34 37
FT HELIX 38 40
FT HELIX 41 42
FT HELIX 43 48
FT HELIX 49 49
FT HELIX 51 53
FT HELIX 54 60
FT STRAND 67 67
FT STRAND 68 68
FT STRAND 70 70
FT STRAND 71 71
FT HELIX 76 79
FT HELIX 82 83
FT HELIX 86 97
FT HELIX 98 98
FT TURN 100 101
FT TURN 104 104
FT TURN 121 122
FT TURN 124 127

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FT HELIX 130 133
FT TURN 134 136
FT STRAND 138 141
FT TURN 138 141
FT STRAND 142 143
FT STRAND 144 147
FT HELIX 148 153
FT TURN 154 154
FT HELIX 154 154
FT HELIX 155 161
FT HELIX 166 182
FT TURN 184 185
FT HELIX 186 193
FT TURN 194 195
FT TURN 198 199
FT HELIX 201 218
FT TURN 219 220
FT TURN 222 223
FT HELIX 226 228
FT STRAND 232 232
FT TURN 234 235
FT HELIX 236 263
SQ SEQUENCE 270 AA; 29327 MM; FA9D25FE75A526EF CRC64;

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Query Match 67.9%; Score 38; DB 1; Length 270;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 NMVKNVGS 10
Db 258 NMVKNVGS 266

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RESULT 20
NUP3_PENSO STANDARD; PRT; 270 AA.
AC P24504;

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DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Nuclease PA3 (EC 3.1.3.6) (Endonuclease PA3) (Deoxyribonuclease PA3).
OS Penicillium sp.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=5081;
RN NCBI_TaxID=5081;
RA SEQUENCE.
RP MEDLINE=91299282; PubMed=1369324;
RA Tabata N., Kazama H., Ohgi K., Irie M.;
RT "Primary structure of a nuclease (nuclease PA3) from a Penicillium
sp."
RL Agric. Biol. Chem. 55:461-469(1991).
RN [2]
RP SEQUENCE OF 1-30 AND 268-270.
RX MEDLINE=91199319; PubMed=1964878;
RA Kazama H., Tabata N., Ohgi K., Irie M.;
RT "Purification and characterization of a nuclease (3'-nucleotidase)
from a Penicillium sp."
RL Chem. Pharm. Bull. 38:3081-3085(1990).
CC -1- FUNCTION: Hydrolyzes only single stranded DNA and RNA without
apparent specificity for bases.
CC -1- CATALYTIC ACTIVITY: A 3'-ribonucleotide + H(2)O = a ribonucleoside
+ phosphate.
CC -1- COFACTOR: BINDS 3 ZINC IONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: TO A.ORYZAE NUCLEASE SL, AND BARLEY NUCLEASE.
DR PIR: J00408; J00408.
DR HSP: P24289; IAKO.
DR InterPro: IPR003154; SI/Plnuclease.
DR Pfam: PF02265; Nuclease_1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; zinc.
FT DISULFID 72 217
FT BY SIMILARITY.
FT CARBOHYD 92 85
FT BY SIMILARITY.
FT CARBOHYD 92 92
FT N-LINKED (GLCNAC. . .).
FT CARBOHYD 138 138
FT N-LINKED (GLCNAC. . .).

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FT CARBOHYD 184 184
FT CARBOHYD 197 197
FT METAL 1 1
FT METAL 6 6
FT METAL 45 45
FT METAL 60 60
FT METAL 116 116
FT METAL 120 120
FT METAL 126 126
FT METAL 149 149
FT METAL 153 153
SQ SEQUENCE 270 AA; 29215 MM; EF52CFDBBA4F16EF CRC64;

```

```

Query Match 67.9%; Score 38; DB 1; Length 270;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 2 NMVKNVGS 10
Db 258 NMVKNVGS 266

```

```

RESULT 21
HDFR_SALTY STANDARD; PRT; 278 AA.
ID HDFR_SALTY
AC Q9L6T4; Q82336;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcriptional regulator hdtR (H-NS-dependent flhdc regulator).
GN HDFR OR STM3897 OR STM01.99 OR STY3708 OR T3449.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN NCBI_TaxID=602, 601;
RA SEQUENCE FROM N.A.
RP SPECIES=S.typhimurium; STRAIN=LT2 / SSGC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McElland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portwoll S., Ali J., Dantle M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RP SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Barrer J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
RP SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G., III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blatter F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Negatively regulates the transcription of the flagellar

```



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CC master operon flhdc by binding to the upstream region of the
CC operon (by similarity).
CC -1 SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC -----
CC EMBL: AE008882; ALU22747.1; ALT_INIT.
CC DR EMBL: AF233324; AAF348.1; ALT_INIT.
CC DR EMBL: AL627279; CAD09467.1; -.
CC DR EMBL: AE016845; AAO70970.1; -.
CC DR STyGene: SC72727; hfr.
CC DR HAMAP: MF_01233; -.
CC DR InterPro: IPR000847; HTH_LYSR.
CC DR InterPro: IPR005119; LYSR_subst.
CC DR Pfam: PF00126; HTH_1; 1.
CC DR Pfam: PF03466; LYSR_substrate; 1.
CC DR PRINTS: PR00039; HTHLYSR.
CC DR PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC DR Transcription regulation; Repressor: DNA-binding; Complete proteome.
CC DNA_BIND 18 H-T-H MOTIF (BY SIMILARITY).
CC SEQUENCE 278 AA; 31604 MW; 68B85DF1530CE0CB CRC64;
SQ
Query Match 67.9%; Score 38; DB 1; Length 278;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 VNMVKNKVG 9
DB 230 VNMANKG 238

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CC -----
CC EMBL: X53049; CAJ37217.1; -.
CC DR EMBL: X73301; CA51734.1; -.
CC DR PIR: S10514; S10514.
CC DR HSSP: P04063; JAVA.
CC DR InterPro: IPR006589; Alp_amy1_cat_sub.
CC DR InterPro: IPR006047; Alpha_amy1_cat.
CC DR InterPro: IPR006046; Glyco_hydro_13.
CC DR Pfam: PF00128; alpha-amy1ase; 1.
CC DR PRINTS: SM00642; Amyy; 1.
CC DR SMART: SM00642; Amyy; 1.
CC KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Calcium; signal.
CC FT SIGNAL 1 23 PROBABLE.
CC FT CHAIN 24 421 ALPHA-AMYLASE.
CC FT ACT_SITE 201 201 BY SIMILARITY.
CC FT ACT_SITE 309 309 BY SIMILARITY.
CC FT METAL 113 113 CALCIUM (BY SIMILARITY).
CC FT METAL 172 172 CALCIUM (BY SIMILARITY).
CC SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;
SQ
Query Match 67.9%; Score 38; DB 1; Length 421;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 VNMVKNKVG 10
DB 251 VNMVNSNGA 260

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RESULT 22
ID AMYA_VICMU STANDARD: PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amy1ase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram);
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colyleodon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amy1ase from cotyledons of
RT germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT Nucleotide sequence of the alpha-amy1ase gene from Vigna mungo.;
RL Plant Physiol. 103:1459-1459(1993).
CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1 COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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RESULT 23
ID RPOB_ARATH STANDARD: PRT; 1072 AA.
AC P50546;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
GN RPOB OR ATCG00190.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Leaf;
RX MEDLINE=20069369; PubMed=10601874;
RA Pfannschmidt T., Ojzewska K., Baginski S., Sickmann A., Meyer H.E.,
RA Link G.;
RT The multisubunit chloroplast RNA polymerase A from mustard (Sinapis
RT alba L.). Integration of a prokaryotic core into a larger complex
RT with organelle-specific functions.;
RL Eur. J. Biochem. 267:253-261(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20039611; PubMed=10574454;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
RT thaliana.";
RL DNA Res. 6:283-290(1999).
RN [3]
RP SEQUENCE OF 346-713 FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE=Cotyledon;
RA Knut J., Pfannschmidt T., Liere K., Link G.;

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RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
DR EMBL: Y13690; CAA74024.1; ALT_INT.
DR EMBL: AP000423; BAA84377.1; -.
DR EMBL: X84159; CAA58965.1; -.
DR PIR: S52324; S52324.
DR HSSP: O9KWU7; IHOM.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam: PF00562; RNA_pol_Rpb2_6; 2.
DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
DR Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
KM CONFLICT 286 286 I -> V (IN REF. 2).
FT CONFLICT 341 341 G -> S (IN REF. 2).
FT CONFLICT 346 346 Y -> H (IN REF. 2).
FT CONFLICT 599 599 L -> F (IN REF. 2).
FT CONFLICT 927 927 T -> S (IN REF. 2).
FT CONFLICT 958 959 VI -> DK (IN REF. 2).
FT CONFLICT 1038 1038 Q -> P (IN REF. 2).
SQ SEQUENCE 1072 AA; 121049 MW; A66DD28ED666FABA CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1072;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNVKVGGS 10
Db 790 VRWVQKKGGS 799

RESULT 24
PROB_SAPOF STANDARD; PRT; 1078 AA.
ID PROB_SAPOF
AC P46818; O9THV7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
GN RPOB.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_TaxID=3728;
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
RC STRAIN=cv. albatros; TISSUE=cotyledon;
RA MEDLINE=200636369; PubMed=10601874;
RA Pflanschmidt T., Ogrzewalla K., Baginsky S., Sickmann A., Meyer H.E.,
RA Link G.;
RT "The multisubunit chloroplast RNA polymerase A from mustard (Sinapis
RT alba L.). Integration of a prokaryotic core into a larger complex

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RT with organelle-specific functions.";
RL Eur. J. Biochem. 267:253-261(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
DR EMBL: X82417; CAA57814.1; -.
DR EMBL: AJ243754; CAB48411.1; -.
DR PIR: S48842; S48842.
DR HSSP: O9KWU7; IHOM.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam: PF00562; RNA_pol_Rpb2_6; 2.
DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE: PS01166; RNA_POL_BETA; 1.
DR Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
KM CONFLICT 4 4 A -> S (IN REF. 1; CAA57814).
SQ SEQUENCE 1078 AA; 121653 MW; B0C0F2367526DBF8 CRC64;

Query Match 67.9%; Score 38; DB 1; Length 1078;
Best Local Similarity 70.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VNMVNVKVGGS 10
Db 796 VRWVQKKGGS 805

RESULT 25
PROB_SAPOF STANDARD; PRT; 417 AA.
ID PROB_SAPOF
AC P08036;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Fragment).
GN RPOB.
OS Saponaria officinalis (Common soapwort).
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Caryophyllidae; Caryophyllales; Caryophyllaceae; Saponaria.
OX NCBI_TaxID=3572;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RA MEDLINE=88217525; PubMed=3368320;
RA Benatti L., Lorenzetti R., Dani M., Martini D., Minganti C.,
RA Sasano M., Siodoli A., Sorla M.;
RT "A DNA sequence from Saponaria officinalis is similar to various RNA
RT polymerase genes.";
RL Nucleic Acids Res. 16:3103-3103(1988).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).

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CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
CC EMBL: X07026; CA930075.1; -
CC PIR: S00933; S00933.
CC HSSP: G9KM07; IHQM.
CC InterPro: IPR001572; RNA_pol_B.
CC Pfam: PF00562; RNA_pol_Rpb2_6; 1.
CC PROSITE: PS01166; RNA_POL_BETA; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
CC NON_TER 1 1
CC FT NON_TER 417 417
CC SEQUENCE 417 AA; 46637 MW; 2AF853B23B35A8 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 417;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 VNMVKNKVGGS 10
DB 230 VNMVKNKVGGS 239

RESULT 26
R114_SACPA STANDARD; PRT; 432 AA.
AC P78956;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Meiotic recombination protein REC114.
GN REC114.
OS Saccharomyces paradoxus (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=27291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBGV 6466 / CBS 5829;
RX MEDLINE=97412794; PubMed=9267437;
RA Malone R.E., Pittman D.L., Nau J.J.;
RA "Examination of the Intron in the meiosis-specific recombination gene
RT REC114 in Saccharomyces";
RL Mol. Gen. Genet. 255:410-419(1997).
CC -1- FUNCTION: REQUIRED FOR MEIOTIC RECOMBINATION EVENTS; NOT REQUIRED
CC FOR MIOSIS.
CC -1- DEVELOPMENTAL STAGE: MEIOSIS-SPECIFIC.
CC -----
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CC -----
CC EMBL: Y08767; CA970020.1; -
CC InterPro: IPR004354; Meiotic_rec114.
CC Pfam: PF03525; Meiotic_rec114; 1.
CC PRINTS: PR01548; MEIOTICR114.
CC PRODOM: PD025162; Meiotic_rec114; 1.
CC MEIOSIS.
CC SEQUENCE 432 AA; 48921 MW; C53AF897B943075D CRC64;

Query Match 66.1%; Score 37; DB 1; Length 432;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 VNMVKNV 7
DB 416 MNMVKV 422

RESULT 27
RPOB_SPTOL STANDARD; PRT; 1070 AA.
AC P11703;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
GN RPOB.
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88316931; PubMed=3045324;
RA Hudson G.S., Holton T.A., Whitfield P.R., Bottomley W.;
RA "Spinach chloroplast rpoB genes encode three subunits of the
RT chloroplast RNA polymerase";
RL J. Mol. Biol. 200:639-654(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Geant d'hiver, and cv. Monatoli;
RX MEDLINE=21187424; PubMed=11292076;
RA Schmitz-Lineweber C., Maier R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Mache R.;
RA "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization";
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -1- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
CC subunits: alpha, beta, beta', and beta".
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
CC EMBL: AJ400848; CAB88717.1; -
CC PIR: C28959; C28959.
CC HSSP: G9KM07; IHQM.
CC InterPro: IPR001572; RNA_pol_B.
CC Pfam: PF04563; RNA_pol_Rpb2_1; 1.
CC Pfam: PF04561; RNA_pol_Rpb2_2; 1.
CC Pfam: PF04565; RNA_pol_Rpb2_3; 1.
CC Pfam: PF00562; RNA_pol_Rpb2_6; 2.
CC Pfam: PF04560; RNA_pol_Rpb2_7; 1.
CC PROSITE: PS01166; RNA_POL_BETA; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription; Chloroplast.
CC SEQUENCE 1070 AA; 120899 MW; 8BA809389BA421F9 CRC64;

Best Local Similarity 60.0%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy 1 VNMVKNYGG 10
1 1 1 1 1
Db 788 VNMVKNYGG 797

RESULT 28
ID YECP_HAEIN STANDARD; PRT; 321 AA.
AC P44167;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein H11351.
GN H11351.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=127;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McMenemy K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
Fine L.D., Fitchman J.L., Fuhmann J.L., Geoghegan N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000)
CC -I- SIMILARITY: STRONG, TO E.COLI YECP.

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CC EMBL: U32814; AAC22998.1; -
CC PIR: E64026; E64026.
CC TIGR: H11351; -
CC InterPro: IPR000051; SAM_bind.
KW Complete proteome.
SQ SEQUENCE 321 AA; 36854 MW; 6CC25B67E4F5995A CRC64;

Query Match 64.3%; Score 36; DB 1; Length 321;
Best Local Similarity 62.3%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VNMVKNYGG 8
1 1 1 1 1
Db 258 INMIEKVG 265

RESULT 29
AM3C_ORYSA STANDARD; PRT; 437 AA.
ID AM3C_ORYSA
DT 01-AUG-1992 (Rel. 23, Last sequence update)

AC P27939;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMY1.7 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Japonica M202; TISSUE-Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -I- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -I- SUBUNIT: Monomer.
CC -I- TISSUE SPECIFICITY: GERMINATING SEEDS.
CC -I- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALEURONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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CC EMBL: X56338; CAA39778.1; -
CC PIR: S14956; S14956.
CC HSSP: P04063; JAVa.
CC DR Gramene; P27939; -
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC Pfam: PF00128; alpha-amylase; 1.
CC SMART: SM00642; Amy; 1.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 437
FT ACT_SITE 205 205
FT ACT_SITE 313 313
FT METAL 117 117
FT METAL 176 176
SQ SEQUENCE 437 AA; 48637 MW; BD304230B40C7A8B CRC64;
Query Match 64.3%; Score 36; DB 1; Length 437;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 1 VNMVKNYGG 9
1 1 1 1 1
Db 255 VNMVKNYGG 263

RESULT 30
AM3B_ORYSA STANDARD; PRT; 438 AA.
ID AM3B_ORYSA
AC P27937;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)

```

DR 15-SEP-2003 (rel. 42, last annotation update)
DE Alpha-amylase isozyme 3b precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
GN glucanohydrolase).
OS AM1.6 OR AM13B.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophoridae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Sutcliffe T.D., Huang N., Rodriguez R.L.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING
CC GERMINATION.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: GERMINATING SEEDS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION
CC IN THE ALBURNONS CELLS UNDER THE CONTROL OF THE PLANT HORMONE
CC GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X56337; CAA39777.1; -
DR EMBL: M24941; AAA3897.1; -
DR PIR: S14957; S14957.
DR HSSP: P04063; IAVA.
DR Gramene: P27937; -.
DR InterPro: IPR006589; Alp_ami1_cat_sub.
DR InterPro: IPR006047; Alpha_ami1_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 438 ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 205 205 BY SIMILARITY.
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 117 117 CALCIUM (BY SIMILARITY).
FT METAL 176 176 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 438 AA; 48591 MW; B9DE0DB5ABC63F9C CRC64;
Query Match 64.3%; Score 36; DB 1; Length 438;
Best Local Similarity 66.7%; Pred. NO. 51;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 VNMVNRKVG 9
DB 255 VNMVAQVGG 263

```

Search completed: August 29, 2003, 18:45:14
 Job time : 8.57143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2003, 18:40:26 ; Search time 24.5714 Seconds

(without alignments)
105.021 Million cell updates/sec

Title: US-09-830-876-3

Perfect score: 56

Sequence: 1 VMWNVKVGGS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 56 | 100.0 | 28 | 10 Q42364 | Q42364 triticum ae |
| 2 | 56 | 100.0 | 427 | 10 Q03651 | Q03651 hordeum vul |
| 3 | 56 | 100.0 | 429 | 10 Q40016 | Q40016 hordeum vul |
| 4 | 50 | 89.3 | 424 | 10 Q94DK9 | Q94DK9 oryza sativ |
| 5 | 48 | 85.7 | 29 | 10 Q42365 | Q42365 triticum ae |
| 6 | 48 | 85.7 | 421 | 10 Q42504 | Q42504 hordeum vul |
| 7 | 48 | 85.7 | 437 | 10 Q04964 | Q04964 hordeum vul |
| 8 | 48 | 85.7 | 437 | 10 Q04965 | Q04965 hordeum vul |
| 9 | 48 | 85.7 | 438 | 10 Q40017 | Q40017 hordeum vul |
| 10 | 47 | 83.9 | 427 | 10 Q40015 | Q40015 hordeum vul |
| 11 | 47 | 83.9 | 437 | 10 Q40018 | Q40018 hordeum vul |
| 12 | 42 | 75.0 | 416 | 10 Q8LJ06 | Q8LJ06 musa acumin |
| 13 | 42 | 75.0 | 416 | 10 Q8GUR0 | Q8GUR0 musa acumin |
| 14 | 41 | 73.2 | 434 | 10 Q81699 | Q81699 avena fatua |
| 15 | 41 | 73.2 | 437 | 10 Q81700 | Q81700 avena fatua |
| 16 | 41 | 73.2 | 709 | 9 Q94MY4 | Q94MY4 haemophilus |

| | | | | | |
|----|----|------|------|------------|---------------------|
| 17 | 40 | 71.4 | 136 | 12 Q8V211 | Q8V211 camelus vir |
| 18 | 40 | 71.4 | 139 | 15 Q04144 | Q04144 bovine immu |
| 19 | 40 | 71.4 | 340 | 12 Q57262 | Q57262 vaccinia vi |
| 20 | 40 | 71.4 | 340 | 12 Q8QNM7 | Q8QNM7 cowpox viru |
| 21 | 40 | 71.4 | 340 | 12 Q72752 | Q72752 cowpox viru |
| 22 | 40 | 71.4 | 340 | 12 Q9JFE7 | Q9JFE7 ectromelia |
| 23 | 40 | 71.4 | 340 | 12 Q9JFE36 | Q9JFE36 vaccinia vi |
| 24 | 40 | 71.4 | 875 | 15 Q65597 | Q65597 bovine immu |
| 25 | 39 | 69.6 | 157 | 16 Q92AAS | Q92AAS listeria in |
| 26 | 39 | 69.6 | 157 | 16 Q8Y600 | Q8Y600 listeria mo |
| 27 | 39 | 69.6 | 397 | 17 Q9YD25 | Q9YD25 aeropyrum p |
| 28 | 39 | 69.6 | 472 | 17 Q8ZX92 | Q8ZX92 pyrobaculum |
| 29 | 39 | 69.6 | 492 | 2 Q8GCK3 | Q8GCK3 mycoplasma |
| 30 | 39 | 69.6 | 548 | 16 Q8Y7M0 | Q8Y7M0 listeria mo |
| 31 | 39 | 69.6 | 937 | 2 Q8GCN3 | Q8GCN3 mycoplasma |
| 32 | 39 | 69.6 | 937 | 2 Q8GCK4 | Q8GCK4 mycoplasma |
| 33 | 38 | 67.9 | 420 | 10 Q9ZP43 | Q9ZP43 phaseolus v |
| 34 | 38 | 67.9 | 555 | 16 Q8XMX6 | Q8XMX6 clostridium |
| 35 | 38 | 67.9 | 627 | 16 Q8YR83 | Q8YR83 arabidopsis |
| 36 | 37 | 66.1 | 132 | 17 Q30054 | Q30054 archaeoglob |
| 37 | 37 | 66.1 | 149 | 2 Q93OM0 | Q93OM0 erythra tra |
| 38 | 37 | 66.1 | 149 | 2 Q93OM4 | Q93OM4 erythra tra |
| 39 | 37 | 66.1 | 228 | 17 Q27733 | Q27733 methanobact |
| 40 | 37 | 66.1 | 252 | 17 Q9HTA0 | Q9HTA0 thermoplasma |
| 41 | 37 | 66.1 | 278 | 10 Q9AKJ3 | Q9AKJ3 arabidopsis |
| 42 | 37 | 66.1 | 346 | 10 Q9SUZ8 | Q9SUZ8 arabidopsis |
| 43 | 37 | 66.1 | 346 | 16 Q8EWM5 | Q8EWM5 mycoplasma |
| 44 | 37 | 66.1 | 439 | 16 Q9HW58 | Q9HW58 pseudomonas |
| 45 | 37 | 66.1 | 455 | 16 Q8ESL2 | Q8ESL2 oceanobacill |
| 46 | 37 | 66.1 | 516 | 5 Q18198 | Q18198 caenorhabdi |
| 47 | 37 | 66.1 | 527 | 16 Q9CJ47 | Q9CJ47 lactococcus |
| 48 | 37 | 66.1 | 574 | 16 Q9KFR82 | Q9KFR82 bacillus ha |
| 49 | 37 | 66.1 | 952 | 3 Q9UVY5 | Q9UVY5 gibberella |
| 50 | 37 | 66.1 | 952 | 3 Q74290 | Q74290 gibberella |
| 51 | 37 | 66.1 | 1070 | 8 Q8HVV5 | Q8HVV5 glycine max |
| 52 | 37 | 66.1 | 1273 | 12 Q9QSK2 | Q9QSK2 chilo iride |
| 53 | 37 | 66.1 | 1280 | 5 Q22554 | Q22554 caenorhabdi |
| 54 | 36 | 64.3 | 1280 | 5 Q05904 | Q05904 mycobacteri |
| 55 | 36 | 64.3 | 160 | 16 Q8RAS4 | Q8RAS4 thermoaer |
| 56 | 36 | 64.3 | 207 | 16 Q8EFL7 | Q8EFL7 shewanella |
| 57 | 36 | 64.3 | 226 | 8 Q94O59 | Q94O59 odontoteme |
| 58 | 36 | 64.3 | 281 | 10 Q94JG6 | Q94JG6 oryza sativ |
| 59 | 36 | 64.3 | 321 | 16 Q9CMT5 | Q9CMT5 pasteurella |
| 60 | 36 | 64.3 | 341 | 2 Q8RJ58 | Q8RJ58 haemophilus |
| 61 | 36 | 64.3 | 344 | 2 Q8RML9 | Q8RML9 haemophilus |
| 62 | 36 | 64.3 | 344 | 2 Q8RML0 | Q8RML0 haemophilus |
| 63 | 36 | 64.3 | 344 | 2 Q8RML1 | Q8RML1 haemophilus |
| 64 | 36 | 64.3 | 344 | 2 Q8RML2 | Q8RML2 haemophilus |
| 65 | 36 | 64.3 | 344 | 2 Q8RML3 | Q8RML3 haemophilus |
| 66 | 36 | 64.3 | 344 | 2 Q8RML4 | Q8RML4 haemophilus |
| 67 | 36 | 64.3 | 344 | 2 Q8RML5 | Q8RML5 haemophilus |
| 68 | 36 | 64.3 | 344 | 2 Q8RML6 | Q8RML6 haemophilus |
| 69 | 36 | 64.3 | 344 | 2 Q8RML7 | Q8RML7 haemophilus |
| 70 | 36 | 64.3 | 344 | 2 Q8RML8 | Q8RML8 haemophilus |
| 71 | 36 | 64.3 | 344 | 2 Q8RML9 | Q8RML9 haemophilus |
| 72 | 36 | 64.3 | 344 | 2 Q8RML0 | Q8RML0 haemophilus |
| 73 | 36 | 64.3 | 344 | 2 Q8RML1 | Q8RML1 haemophilus |
| 74 | 36 | 64.3 | 344 | 2 Q8RML2 | Q8RML2 haemophilus |
| 75 | 36 | 64.3 | 344 | 2 Q8RML3 | Q8RML3 haemophilus |
| 76 | 36 | 64.3 | 344 | 2 Q8RML4 | Q8RML4 haemophilus |
| 77 | 36 | 64.3 | 344 | 2 Q8RML5 | Q8RML5 haemophilus |
| 78 | 36 | 64.3 | 344 | 2 Q8RML6 | Q8RML6 haemophilus |
| 79 | 36 | 64.3 | 344 | 2 Q8RML7 | Q8RML7 haemophilus |
| 80 | 36 | 64.3 | 344 | 2 Q8RML8 | Q8RML8 haemophilus |
| 81 | 36 | 64.3 | 344 | 2 Q8RML9 | Q8RML9 haemophilus |
| 82 | 36 | 64.3 | 344 | 2 Q8RML0 | Q8RML0 haemophilus |
| 83 | 36 | 64.3 | 344 | 2 Q8RML1 | Q8RML1 haemophilus |
| 84 | 36 | 64.3 | 344 | 2 Q8RML2 | Q8RML2 haemophilus |
| 85 | 36 | 64.3 | 344 | 2 Q8RML3 | Q8RML3 haemophilus |
| 86 | 36 | 64.3 | 344 | 2 Q8RML4 | Q8RML4 haemophilus |
| 87 | 36 | 64.3 | 344 | 2 Q8RML5 | Q8RML5 haemophilus |
| 88 | 36 | 64.3 | 344 | 2 Q8RML6 | Q8RML6 haemophilus |
| 89 | 36 | 64.3 | 344 | 2 Q8RML7 | Q8RML7 haemophilus |

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90      36      64.3      589      10      0040091
91      36      64.3      589      10      0940060
92      36      64.3      602      16      08E215
93      36      64.3      664      16      092EG8
94      36      64.3      664      16      08Y9N6
95      36      64.3      702      17      08ZU82
96      36      64.3      1070      10      08S8X9
97      35      62.5      96      5      096106
98      35      62.5      98      6      09T595
99      35      62.5      101      2      08RLX1
100     35      62.5      137      16      08B6T4
004091 arabidopsis
094060 arabidopsis
08E215 lespodista
092EG8 listeria in
08Y9N6 listeria mo
08ZU82 pyrobaculum
08S8X9 atropa bell
096106 reticuliter
09T595 oryctolagus
08RLX1 chlorobium
08B6T4 streptococc

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ALIGNMENTS

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RESULT 1
042364      PRELIMINARY;      PRT;      28 AA.

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AC      042364;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-OCT-2000 (TREMblrel. 15, Last annotation update)
DE      Alpha-amylase subfamily Amy1 protein (Fragment).
OS      Triticum aestivum (wheat).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Triticum.
OX      NCBI_TaxID=4565;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92366494; PubMed=1502164;
RA      Huang N., Stebbins G.L., Rodriguez R.L.;
RT      "Classification and evolution of alpha-amylase genes in plants.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).
DR      EMBL: S42213; AAD13822.1; -
DR      HSSP: P04063; JAVa. 1
FT      NON_TER
SQ      SEQUENCE      28 AA: 3022 MW; 69EB0A4138FA3A1 CRC64;

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Query Match      100.0%; Score 56; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VNMVNVKVGGS 10
      1111111111
DB      5 VNMVNVKVGGS 14

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RESULT 2
003651      PRELIMINARY;      PRT;      427 AA.
AC      003651;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Alpha-amylase precursor (BC 3.2.1.1).
GN      AMY46.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=Himalaya;
RC      MEDLINE=89066691; PubMed=3264283;
RA      Khurshed B., Rogers J.C.;
RT      "Barley alpha-amylase genes. Quantitative comparison of steady-state
RT      mRNA levels from individual members of the two different families
RT      expressed in aleurone cells.";
RL      J. Biol. Chem. 263:18953-18960(1988).
DR      EMBL: J04202; AAA98615.1; -

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DR      HSSP: P04063; JAVa.
DR      InterPro: IPR006047; Alpha-amyl_cat.
DR      InterPro: IPR006589; Alp_amyl_cat_sub.
DR      InterPro: IPR006046; Glyco_hydro_13.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      PRINTS: PR00110; ALPHAAMYLIASE.
DR      SMART: SM00642; Amy; 1.
KW      Glycosidase; Hydrolase; Signal.
FT      SIGNAL
FT      CHAIN      1      25      POTENTIAL.
FT      SEQUENCE      427 AA: 47456 MW; 5A7496B9E6643824 CRC64;

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Query Match      100.0%; Score 56; DB 10; Length 427;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 VNMVNVKVGGS 10
      1111111111
DB      253 VNMVNVKVGGS 262

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```

RESULT 3
040016      PRELIMINARY;      PRT;      429 AA.
ID      040016;
AC      040016;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE      Barley (H.vulgare) alpha-amylase 1.
OS      Hordeum vulgare (Barley).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC      Triticeae; Hordeum.
OX      NCBI_TaxID=4513;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
RT      "Structure and organization of two divergent alpha-amylase genes from
RT      barley";
RL      Plant Mol. Biol. 9:3-17(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Muthukrishnan S.;
RL      Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
DR      EMBL: M17125; AAA32926.1; -
DR      HSSP: P04063; JAVa.
DR      InterPro: IPR006047; Alpha-amyl_cat.
DR      InterPro: IPR006589; Alp_amyl_cat_sub.
DR      Pfam: PF00128; alpha-amylase; 1.
DR      SMART: SM00642; Amy; 1.
SQ      SEQUENCE      429 AA: 47970 MW; 4E7B8B741C944095 CRC64;

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Query Match      100.0%; Score 56; DB 10; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VNMVNVKVGGS 10
      1111111111
DB      255 VNMVNVKVGGS 264

```

```

RESULT 4
094DK9      PRELIMINARY;      PRT;      424 AA.
AC      094DK9;
DT      01-DEC-2001 (TREMblrel. 19, Created)
DT      01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT      01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE      Putative alpha-amylase.
GN      P0514H03.1 OR P0025H06.12.
OS      Oryza sativa (Rice), and
OS      Oryza sativa (Japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  Ehrhartoideae; Oryzeae; Oryza.
OX  NCBI_TaxID=4530, 39947;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  SPECIES-O.saliva; STRAIN=cv. Nipponbare;
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT  clone:P0514H03."
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  SPECIES-O.saliva (japonica cultivar-group); STRAIN=cv. Nipponbare;
RA  Sasaki T., Matsumoto T., Yamamoto K.;
RT  "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT  clone:P0025H06."
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AP003275; BAB3640.1; -.
DR  EMBL; AP003312; BAC10723.1; -.
DR  Gramene; G94DK9; -.
DR  InterPro: IPR006047; Alpha-amyl_cat.
DR  Pfam; PF00128; alpha-amylase; 1.
SQ  SEQUENCE 424 AA; 45862 MW; 228582D57B271692 CRC64;

Query Match      89.3%; Score 50; DB 10; Length 424;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY  1 VNMVKNKVGGS 10
    |||||:||||
DB  130 VNMVKNKVGGA 139

RESULT 5
OY  042365          PRELIMINARY;      PRT;      29 AA.
AC  042365;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT  01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE  Alpha-amylase subfamily Amy2 protein (Fragment).
OS  Triticum aestivum (wheat).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC  Triticeae; Triticum.
OX  NCBI_TaxID=4565;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92366494; Pubmed=1502164;
RA  Huang N., Stebbins G.L., Rodriguez R.L.;
RT  "Classification and evolution of alpha-amylase genes in plants."
RT  Proc. Natl. Acad. Sci. U.S.A. 89:7526-7530(1992).
DR  EMBL; S42217; AAD13823.1; -.
DR  HSSP; P04063; IAVA.
DR  NON_TER
SQ  SEQUENCE 29 AA; 3082 MW; 71FB73013D584A8 CRC64;

Query Match      85.7%; Score 48; DB 10; Length 29;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY  1 VNMVKNKVGGS 10
    |||||:||||
DB  5 VNMVKNKVGGA 14

RESULT 6
OY  042504          PRELIMINARY;      PRT;      421 AA.
AC  042504;
DT  01-NOV-1996 (TREMBLrel. 01, Created)
DT  01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)

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DE  Alpha-amylase type A.
GN  AMY1 OR AMY32B.
OS  Hordeum vulgare (Barley).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OX  NCBI_TaxID=4513;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Whittier R.F., Dean D.A., Rogers J.C.;
RT  Nucleic Acids Res. 13:0-0(1987).
RL  [2]
RP  SEQUENCE OF 146 FROM N.A.
RX  MEDLINE=85006965; Pubmed=6090459;
RA  Rogers J.C., Millman C.;
RT  "Coordinate increase in major transcripts from the high pi alpha-
RT  amylase multigene family in barley aleurone cells stimulated with
RT  gibberellic acid."
RL  J. Biol. Chem. 259:12234-12240(1984).
RN  [3]
RP  SEQUENCE FROM N.A.
RA  Whittier R.F., Dean D.A., Rogers J.C.;
RT  Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
DR  EMBL; X05166; CAA28803.1; -.
DR  EMBL; M15208; AAA32935.1; -.
DR  HSSP; P04063; IAVA.
DR  InterPro: IPR006047; Alpha-amyl_cat.
DR  InterPro: IPR006589; Alp_amyl_cat_sub.
DR  InterPro: IPR006046; Glyco_hydro_13.
DR  Pfam; PF00128; alpha-amylase; 1.
DR  PRINTS; PR00110; ALPHAMYLASE.
DR  SMART; SM00642; Amy; 1.
DR  Glycosidase; Hydrolase.
SQ  SEQUENCE 437 AA; 47776 MW; E163524C8BCB2480 CRC64;

RESULT 7
OY  004964          PRELIMINARY;      PRT;      437 AA.
AC  004964;
DT  01-JUL-1997 (TREMBLrel. 04, Created)
DT  01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Alpha-amylase (EC 3.2.1.1).
OS  Hordeum vulgare (Barley).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC  Triticeae; Hordeum.
OX  NCBI_TaxID=4513;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Matthews P.R., Gubler F., Jacobsen J.V.;
RT  "A plant-based expression system for matching cDNA clones and
RT  isozyms."
RL  Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Y11276; CAA72143.1; -.
DR  HSSP; P04063; IAVA.
DR  InterPro: IPR006047; Alpha-amyl_cat.
DR  InterPro: IPR006589; Alp_amyl_cat_sub.
DR  InterPro: IPR006046; Glyco_hydro_13.
DR  Pfam; PF00128; alpha-amylase; 1.
DR  PRINTS; PR00110; ALPHAMYLASE.
DR  SMART; SM00642; Amy; 1.
DR  Glycosidase; Hydrolase.
SQ  SEQUENCE 437 AA; 47776 MW; E163524C8BCB2480 CRC64;

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Query Match 85.7%; Score 48; DB 10; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
 |||||:||||:
 DB 253 VNMVNRKVGGA 262

RESULT 8

ID 004965 PRELIMINARY; PRT; 437 AA.
 AC 004965;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1).
 GN AMT.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Matthews P.R., Gubler F., Jacobsen J.V.;
 RA "A plant-based expression system for matching cDNA clones and
 RT isozymes."
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y11277; CAA72144.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.
 KW Glycosidase; Hydrolase.
 SQ SEQUENCE 437 AA; 47770 MW; 67E910E7CB7769F4 CRC64;
 Query Match 85.7%; Score 48; DB 10; Length 437;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNMVNRKVGGS 10
 |||||:||||:
 DB 253 VNMVNRKVGGA 262

RESULT 9

ID 040017 PRELIMINARY; PRT; 438 AA.
 AC 040017;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Bailey (H.vulgare) alpha-amylase 2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RA "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 DR EMBL: M17128; AAA32927.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat_sub.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR SMART: SM00642; Amy; 1.

SQ SEQUENCE 438 AA; 47824 MW; 38945AF6DBA2309 CRC64;

Query Match 85.7%; Score 48; DB 10; Length 438;
 Best Local Similarity 80.0%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 10
 |||||:||||:
 DB 254 VNMVNRKVGGA 263

RESULT 10

ID 040015 PRELIMINARY; PRT; 427 AA.
 AC 040015;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE Barley (H.vulgare) alpha-amylase 1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RA "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muthukrishnan S.;
 RL Submitted (JUL-1988) to the EMBL/GenBank/DBJ databases.
 DR EMBL: M17126; AAA32925.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006046; Glyco_hydro_13.
 DR Pfam: PF00128; alpha-amylase; 1.
 DR PRINTS: PR00110; ALPHAMYLASE.
 SQ SEQUENCE 427 AA; 47402 MW; D21BA12EAE5F3534 CRC64;
 Query Match 83.9%; Score 47; DB 10; Length 427;
 Best Local Similarity 88.9%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNMVNRKVGGS 9
 |||||:||||:
 DB 253 VNMVNRKVGGA 261

RESULT 11

ID 040018 PRELIMINARY; PRT; 437 AA.
 AC 040018;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Bailey (H.vulgare) alpha-amylase 2.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxID=4513;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP Knox C.A.P., Sonthayanon B., Chandra G.R., Muthukrishnan S.;
 RA "Structure and organization of two divergent alpha-amylase genes from
 RT barley."
 RL Plant Mol. Biol. 9:3-17(1987).
 DR EMBL: M17127; AAA32928.1; -.
 DR HSSP: P04063; IAVA.
 DR InterPro: IPR006047; Alpha_amyl_cat.

| | |
|-----------------------|--|
| DR | InterPro: IPR006589; Alp-amy1_cat-sub. |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; |
| OC | Musa. |
| OX | NCBI_TaxID=4641; |
| RN | SEQUENCE FROM N.A. |
| RP | STRAIN=cv. Naniçao; TISSUE=leaf; |
| RA | Vieira A. Jr.; Nascimento J.R.O.; Lajolo F.M.; |
| RT | "Sequencing and molecular characterization of a banana alpha-amy1ase |
| RT | cDNA clone related to the fruit ripening"; |
| RL | Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL: AF535648; AAO1149.1; -. |
| DR | InterPro: IPR006047; Alpha-amy1_cat. |
| DR | InterPro: IPR006589; Alp-amy1_cat-sub. |
| DR | InterPro: IPR006046; Glyco_hydro_13. |
| DR | Pfam: PF00128; alpha-amy1ase; 1. |
| DR | PRINTS: PR00110; ALPHAMYLASE. |
| DR | SMART: SM00642; Amy; 1. |
| KW | Signal; Hydrolase; Glycosidase. |
| FT | SIGNAL 1 15 |
| FT | CHAIN 16 416 |
| FT | SEQUENCE 416 AA; 46798 MW; 590CEFA392EECDAS CRC64; |
| SO | SEQUENCE 416 AA; 46798 MW; 590CEFA392EECDAS CRC64; |
| Query Match | 75.0%; Score 42; DB 10; Length 416; |
| Best Local Similarity | 77.8%; Pred. No. 28; |
| Matches | 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0; |
| OY | 1 VNMVNRKVG 9 |
| DB | 244 VNMVQVGVG 252 |
| RESULT 13 | |
| OC | OGURO |
| AC | PRELIMINARY; PRT; 416 AA. |
| DT | 01-MAR-2003 (TREMblrel. 23, Created) |
| DT | 01-MAR-2003 (TREMblrel. 23, Last sequence update) |
| DT | 01-MAR-2003 (TREMblrel. 23, Last annotation update) |
| DE | Alpha-amy1ase precursor (EC 3.2.1.1). |
| OS | Musa acuminata (Banana). |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; |
| OC | Musa. |
| OX | NCBI_TaxID=4641; |
| RN | SEQUENCE FROM N.A. |
| RP | STRAIN=cv. Naniçao; TISSUE=fruit; |
| RA | Vieira A. Jr.; Nascimento J.R.O.; Lajolo F.M.; |
| RT | "Sequencing and molecular characterization of the alpha-amy1ase cDNA |
| RT | expressed during maturation of the banana (Musa spp.)"; |
| RL | Thesis (2001), Universidade de Sao Paulo, Sao Paulo, Brasil. |
| RN | 12] |
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN=cv. Naniçao; TISSUE=fruit; |
| RA | Vieira A. Jr.; Nascimento J.R.O.; Lajolo F.M.; |
| RT | "Sequencing and molecular characterization of a banana alpha-amy1ase |
| RT | cDNA clone related to the fruit ripening"; |
| RL | Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL: AF535648; AAO1149.1; -. |
| DR | InterPro: IPR006047; Alpha-amy1_cat. |
| DR | InterPro: IPR006589; Alp-amy1_cat-sub. |
| DR | InterPro: IPR006046; Glyco_hydro_13. |
| DR | Pfam: PF00128; alpha-amy1ase; 1. |
| DR | PRINTS: PR00110; ALPHAMYLASE. |
| DR | SMART: SM00642; Amy; 1. |
| KW | Signal; Hydrolase; Glycosidase. |
| FT | SIGNAL 1 15 |
| FT | CHAIN 16 416 |
| FT | SEQUENCE 416 AA; 46798 MW; 590CEFA392EECDAS CRC64; |
| SO | SEQUENCE 416 AA; 46798 MW; 590CEFA392EECDAS CRC64; |
| Query Match | 75.0%; Score 42; DB 10; Length 416; |
| Best Local Similarity | 77.8%; Pred. No. 28; |
| Matches | 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0; |
| OY | 1 VNMVNRKVG 9 |
| DB | 244 VNMVQVGVG 252 |
| RESULT 14 | |
| OC | OGURO |
| AC | PRELIMINARY; PRT; 434 AA. |
| ID | 081699; |
| AC | 081699; |
| DT | 01-NOV-1998 (TREMblrel. 08, Created) |
| DT | 01-NOV-1998 (TREMblrel. 08, Last sequence update) |
| DT | 01-MAR-2003 (TREMblrel. 23, Last annotation update) |
| DE | Alpha-amy1ase precursor (EC 3.2.1.1). |
| GN | ALPHA-AMY2A. |
| OS | Avena fatua. |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| OC | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; |
| OC | Avenae; Avena. |
| OX | NCBI_TaxID=4499; |
| RN | SEQUENCE FROM N.A. |
| RP | Willmott R.L.; |
| RA | Willmott R.L.; |
| RL | Thesis (1994), University of Bristol. |
| RN | 12] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=99077315; PubMed=9862499; |
| RA | Willmott R.L.; Rushon P.J.; Hooley R.; Lazarus C.M.; |
| RT | "Dnsel footprints suggest the involvement of at least three types of |
| RT | transcription factors in the regulation of alpha-Amy2A by |
| RT | gibberellin."; |
| RT | Plant Mol. Biol. 38:817-825(1998). |
| DR | EMBL: AJ010728; CA09323.1; -. |
| DR | HSSP: P04063; IAVA. |
| DR | InterPro: IPR006047; Alp-amy1_cat. |
| DR | InterPro: IPR006589; Alp-amy1_cat-sub. |
| DR | InterPro: IPR006046; Glyco_hydro_13. |
| DR | Pfam: PF00128; alpha-amy1ase; 1. |
| DR | PRINTS: PR00110; ALPHAMYLASE. |
| DR | SMART: SM00642; Amy; 1. |
| KW | Glycosidase; Hydrolase; Signal. |
| FT | SIGNAL 1 23 |
| FT | CHAIN 24 434 |
| FT | SEQUENCE 434 AA; 47642 MW; 499P8C3B9767C1E1 CRC64; |
| SO | SEQUENCE 434 AA; 47642 MW; 499P8C3B9767C1E1 CRC64; |
| Query Match | 73.2%; Score 41; DB 10; Length 434; |
| Best Local Similarity | 70.0%; Pred. No. 44; |
| Matches | 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0; |
| OY | 1 VNMVNRKVG 10 |
| DB | 253 VNMVQVGVG 262 |

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RESULT 15
ID 081700 PRELIMINARY; PRT; 437 AA.
AC 081700;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Alpha-amylose precursor (EC 3.2.1.1).
GN ALPHA-AMY2D.
OS Avena fatua.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Avenae; Avena.
OX NCBI_TaxID=4499;
RN [1]
RP SEQUENCE FROM N.A.
RL Willmott R.L.; University of Bristol.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077315; PubMed=9862499;
RA Willmott R.L., Rushton P.J., Hookey R., Lazarus C.M.;
RT "DnaaseI footprints suggest the involvement of at least three types of
RT transcription factors in the regulation of alpha-Amy2/A by
RT glaberrima."
RL Plant Mol. Biol. 38:817-825(1998).
DR EMBL: AJ010729; CAA09324.1; -.
DR HSSP: P04063; IAVA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylose; 1.
DR PRINTS: PR00110; ALPHA-AMYLOSE.
DR SMART: SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 26
FT CHAIN 27 437 POTENTIAL.
FT SEQUENCE 437 AA; 48103 MW; 88CEP3095737589A CRC64;
SQ
Query Match 73.2%; Score 41; DB 10; Length 437;
Best Local Similarity 70.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VNVNKKVGS 10
Db 256 VNVWGVGGA 265

RESULT 16
ID 094MY4 PRELIMINARY; PRT; 709 AA.
AC 094MY4;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Orl27.
GN ORE27.
OS Haemophilus phage HP2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=157239;
RN [1]
RP SEQUENCE FROM N.A.
RA Williams B.J., Golomb M., Olson M.V., Smith A.L.;
RT "The HP2 genome of Haemophilus influenzae."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY027935; AAK37811.1; -.
DR InterPro: IPR006126; StaphStrept-tox.
DR PROSITE: PS00277; STAPH-STREPT_TOXIN_1; 1.
SQ SEQUENCE 709 AA; 75730 MW; A00DB1DCF68802A9 CRC64;
QY
Query Match 73.2%; Score 41; DB 9; Length 709;
Best Local Similarity 73.0%; Pred. No. 73;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 NMVNVKVG 9
Db 166 NMVNVKVG 173

RESULT 17
ID 08V211 PRELIMINARY; PRT; 136 AA.
AC 08V211;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Hypothetical 16.3 kDa protein (CMP193L).
GN CMP193L.
OS Camel痘 virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=203174;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-96;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L.,
RA Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;
RT "The genome of camel痘 virus."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CMS;
RX PubMed=11907336;
RA Gubser C., Smith G.L.;
RT "The sequence of camel痘 virus shows it is most closely related to
RT variola virus, the cause of smallpox."
RL J. Gen. Virol. 83:855-872(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CMS;
RA Gubser C., Smith G.L.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF438165; AAL73905.1; -.
DR EMBL: AY009089; AAG37702.1; -.
KW Hypothetical protein
SQ SEQUENCE 136 AA; 16302 MW; CF62496C588D54CF CRC64;
QY 2 NMVNVKVG 10
Db 96 NMVNVKVG 104

RESULT 18
ID 004144 PRELIMINARY; PRT; 159 AA.
AC 004144;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Rev protein 2.
GN REV2.
OS Bovine immunodeficiency-like virus.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11647;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91251255; PubMed=1645801;
RA Oberste M.S., Greenwood J.D., Gonda M.A.;
RT "Analysis of the transcription pattern and mapping of the putative rev
RT and env splice junctions of bovine immunodeficiency-like virus."
RL J. Virol. 65:3932-3937(1991).

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DR EMBL: M74712: AAA42773.1: -
SQ SEQUENCE 159 AA; 18002 MW; 4DDA6ECB94626C2E CRC64;
Query Match 71.4%; Score 40; DB 15; Length 159;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 MWVNRVGS 10
DB 43 MWLNKRGGS 51
RESULT 19
ID 057262 PRELIMINARY; PRT; 340 AA.
AC 057262;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Putative 39.6k protein.
GN MVA195L.
OS Vaccinia virus (strain Ankara).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=126794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Ankara.
RA Antoine G., Scheiflinger F., Falkner F.G., Dörner F.;
RT "The complete genomic sequence of the Modified Vaccinia Ankara (MVA)
RL strain".
DR EMBL: U94848; AAB96481.1; -
SQ SEQUENCE 340 AA; 39566 MW; DA944A21A712FFB7 CRC64;
Query Match 71.4%; Score 40; DB 12; Length 340;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 MWVNRVGS 10
DB 96 MWVSKVGS 104
RESULT 20
ID 080M7 PRELIMINARY; PRT; 340 AA.
AC 080M7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE V201.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red.
RA MEDLINE=83117629; PubMed=6961398;
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT repeated and unique sequence elements".
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red.
RA MEDLINE=90177240; PubMed=2309453;
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
RL infection".
RN [3]
VIROLOGY 175:69-80(1990).

RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red;
RX MEDLINE=91196263; PubMed=2014645;
RA Hu F.Q., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA is
RT initiated from the telomere sequences directing DNA resolution".
RL Virology 181:716-720(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red;
RX MEDLINE=94378510; PubMed=8091665;
RA Hu F.Q., Smith C.A., Pickup D.J.;
RT "Cowpox virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor".
RL Virology 204:343-356(1994).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red;
RA Pickup D.J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-Brighton Red;
RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF482758; AAM13649.1; -
SQ SEQUENCE 340 AA; 39662 MW; A13ACEFF851CF62 CRC64;
Query Match 71.4%; Score 40; DB 12; Length 340;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 MWVNRVGS 10
DB 96 MWVSKVGS 104
RESULT 21
ID 072752 PRELIMINARY; PRT; 340 AA.
AC 072752;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE B15L protein.
GN B15L.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRI-90;
RX MEDLINE=98229462; PubMed=9568042;
RA Shchelkunov S.N., Safironov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox and vaccinia viruses".
RL Virology 243:432-460(1998).
DR EMBL: Y15035; CA875291.1; -
SQ SEQUENCE 340 AA; 39489 MW; CAEBE1F3089627D3 CRC64;
Query Match 71.4%; Score 40; DB 12; Length 340;
Best Local Similarity 77.8%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 MWVNRVGS 10
DB 96 MWVSKVGS 104
RESULT 22
O9JFS7

ID 09JES7 PRELIMINARY; PRT: 340 AA.
 AC 09JFS7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 101.
 GN C101.
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=12643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOSCOW;
 RC MEDLINE=20192152; PubMed=10725549;
 RA Chen N., Buller R.M.L., Wall E.M., Upton C.;
 RT "Analysis of host response modifier ORFs of ectromelia virus, the
 RT causative agent of mousepox.";
 RL Virus Res. 66:155-173(2000).
 DR EMBL: AF012825; AAC95569.1; -
 SQ SEQUENCE 340 AA; 39636 MW; 29414769AA1EAC49 CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 96 NMVSKVGDS 104

RESULT 23
 09JFS6 PRELIMINARY; PRT: 340 AA.
 AC 09JFS6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 101.
 GN TBI17.
 OS Vaccinia virus (strain Tian Tan).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tian Tan;
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
 RT "Complete genomic sequence of vaccinia virus (Tian Tan strain).";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF095689; AAF34088.1; -
 SQ SEQUENCE 340 AA; 39481 MW; CEALC9CBDF3462AC CRC64;

Query Match 71.4%; Score 40; DB 12; Length 340;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 96 NMVSKVGDS 104

RESULT 24
 065597 PRELIMINARY; PRT: 875 AA.
 AC 065597;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 101-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN ENV.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11647;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=29;
 RA Nadin-Davis S.A., Chang S.C., Roth J.A., Carpenter S.;
 RT "Isolation and characterization of cDNAs encoding rev and tat of
 RT bovine immunodeficiency-like virus.";
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04972; AAA42771.1; -
 DR InterPro: IPR001064; Crystal1in.
 DR InterPro: IPR002114; HPr_Serp_site.
 DR PROSITE: PS00225; CRYSTALIN_BETAGAMMA; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; 1.
 SQ SEQUENCE 875 AA; 99108 MW; 0FA8D362A7FD7EF3 CRC64;

Query Match 71.4%; Score 40; DB 15; Length 875;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVGGS 10
 Db 759 NMVKNIGES 767

RESULT 25
 092AA5 PRELIMINARY; PRT: 157 AA.
 AC 092AA5;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 101-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN Hypothetical protein lin2017.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / Serovar 6a;
 RX PubMed=11679669;
 RA Glaser P., Franjeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussutget O.,
 RA Ertian K.-D., Esli H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkai G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjati H.,
 RA Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.;
 RT "Comparative genomics of Listeria species.";
 RL Science 294:849-852(2001).
 DR EMBL: AL596170; CAC97247.1; -
 DR Listlist: LIN2017;
 DR InterPro: IPR006663; ThioRedox_dom2.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 157 AA; 17707 MW; C0F858787c36E65 CRC64;

Query Match 69.6%; Score 39; DB 16; Length 157;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NMVNVKVG 9
 Db 146 NMVNVKVG 153

RESULT 26
 081600 PRELIMINARY; PRT: 157 AA.
 AC 081600;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
GN LMO1903.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glasier P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
Bagueur F., Berche P., Blocher H., Brandt P., Chakraborty T.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
Ertler K.-D., Fajli H., Garcia-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kunz M., Kunst F., Kurapat G.,
Madueno E., Maizouran A., Mata Vicente J., Ng E., Nedjari H.,
Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Furcell R.,
Reimel B., Rose M., Schlueter T., Simoes N., Cossart P.,
Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.,
RT Comparative genomics of *Listeria species*.
RI Science 294:849-852(2001).
DR EMBL: AL591981; CAC9981.1; -.
DR ListList; LMO01903; -.
DR InterPro: IPR006663; ThioRedox_dom2.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17618 MW; B434208F88C9DE2 CRC64;

Query Match 69.6%; Score 39; DB 16; Length 157;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VMVNVKVG 9
DB 146 VMVNVKVG 153

RESULT 27
OYD5 PRELIMINARY; PRT; 397 AA.
ID O9YD5;
AC O9YD5;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Hypothetical protein APE0774.
GN APE0774.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hakawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,
RA Hosogawa K., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takanuma H., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Nakamura Y., Nomura N., Sako T., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
KT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000060; BAA79752.1; -.
DR InterPro: IPR002052; N6_Mtase.
DR PROSITE: PS00092; N6_MTASE; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 397 AA; 41172 MW; 6E2862BECF406C61 CRC64;

Query Match 69.6%; Score 39; DB 17; Length 397;
Best Local Similarity 55.6%; Pred. No. 90;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VMVNVKVG 9
DB 167 VMVNVKVG 175

RESULT 28
O8ZX92 PRELIMINARY; PRT; 472 AA.
ID O8ZX92
AC O8ZX92;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 23, last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Branched-chain amino acid binding protein.
GN PA03392.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteales; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum."
RT Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
RL EMBL: AE009819; AAL63457.1; -.
DR InterPro: IPR002965; P-rich_extensn.
DR PRINTS: PR01217; PRICEXTENS.
KW Complete proteome.
SQ SEQUENCE 472 AA; 51167 MW; 041175B8A05E70F CRC64;

Query Match 69.6%; Score 39; DB 17; Length 472;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VMVNVKVG 9
DB 102 VMVNVKVG 110

RESULT 29
O8GCK3 PRELIMINARY; PRT; 492 AA.
ID O8GCK3;
AC O8GCK3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
DE ICEF-II ORE17 (Fragment).
OS Mycoplasma fermentans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2115;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PC18;
RX MEDLINE=22336318; PubMed=12446643;
RA Calcutt M.J., Lewis M.S., Wise K.S.;
RT "Molecular Genetic Analysis of ICEF, an Integrative Conjugal Element
RT That is Present as a Repetitive Sequence in the Chromosome of
RL Mycoplasma fermentans PC18."
J. Bacteriol. 184:6929-6941(2002).
DR EMBL: AY168965; AAN85277.1; -.
FT NON_TER
SQ SEQUENCE 492 AA; 55875 MW; B37487ADF79F3783 CRC64;

Query Match 69.6%; Score 39; DB 2; Length 492;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VMVNVKVG 9

DB 124 VKMANKGG 132

RESULT 30

08Y7M0 PRELIMINARY; PRT; 548 AA.
 AC 08Y7M0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein lmo1254.
 GN lmo1254.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
 Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 Ertian K.-D., Pshi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kurapkai G.,
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Roland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of Listeria species."
 RL Science 294:849-852(2001).
 DR EMBL; AL591978; CAC9332.1; -
 DR ListLib; LMO01254; -
 DR InterPro: IPR006047; Alpha_amyl_cat.
 DR InterPro: IPR006589; Alp_amyl_cat-sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 548 AA; 63194 MW; D010A588529197D3 CRC64;

Query Match 69.6%; Score 39; DB 16; Length 548;
 Best Local Similarity 66.7%; Pred. NO. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWYKVGGS 10
 |||:| ||:
 DB 137 NWVSKFSGN 145

Search completed: August 29, 2003, 18:46:51
 Job time : 27.5714 secs

99